

F:387-468/Domain: Intracellular #status predicted <INT>
 F:47-96/Disulfide bonds: #status predicted
 F:55-93/221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 146; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1,6e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 133 EMRPSPTSLTKAVLYKRFNSPAD 160

RESULT 2

Interleukin-6 receptor precursor (clone lambda pL) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000

C:Accession: J01014
 C:Position: 1-1024; T.: Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 F:102-171, 2001-2009, 1990
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gene
 A:Accession: J01014
 A:Accession: J01014; M01D:90278354
 A:Status: nucleic acid sequence not shown

A:Residues: 1-440 <SIG>
 A:Accession: N51976; NID:953548; PIDN:CAA6238.1; PID:953549
 A:Cross-references: GB:X51976; NID:953548; PIDN:CAA6238.1; PID:953549
 A:Superfamily: Cytokine receptor; receptor; cytokine receptor homology; immunog
 A:Keywords: cytokine receptor; receptor; status predicted <SIG>
 F:20-440/Product: Interleukin-6 receptor #status predicted <INT>
 F:40-94/Domain: Immunoglobulin homology <IM>
 F:117-306/Domain: Cytokine receptor homology <CR>
 F:358-385/Domain: transmembrane #status predicted <TR>

Query Match 49.3%; Score 72; DB 2; Length 440;
 Best Local Similarity 58.3%; Pred. No. 0.0037; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Db 129 EMRPSPTSLTKAVLYKRFNS 152

RESULT 3

Interleukin-6 receptor precursor (clone lambda 301) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000

C:Accession: J01015; S14543
 F:102-171, 2001-2009, 1990
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gen
 A:Accession: J01015
 A:Accession: J01015; M01D:90278354
 A:Status: nucleic acid sequence not shown

A:Residues: 1-460 <SIG>
 A:Cross-references: GB:X51976; NID:949725; PIDN:CAA6237.1; PID:949726
 A:Experimental source: clone lambda 301
 A:Accession: J01015; M01D:90278354
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gen
 A:Accession: J01015
 A:Accession: J01015; M01D:90278354
 A:Status: nucleic acid sequence not shown

A:Residues: 1-460 <SIG>
 A:Cross-references: GB:X51976; NID:949725; PIDN:CAA6237.1; PID:949726
 A:Experimental source: clone lambda 301
 A:Accession: J01015; M01D:90278354
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gen
 A:Accession: J01015
 A:Accession: J01015; M01D:90278354
 A:Status: nucleic acid sequence not shown

C:Keywords: cytokine receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-460/Product: Interleukin-6 receptor #status predicted <INT>
 F:40-94/Domain: Immunoglobulin homology <IM>
 F:117-306/Domain: Cytokine receptor homology <CR>
 F:358-385/Domain: transmembrane #status predicted <TR>

Query Match 49.3%; Score 72; DB 2; Length 460;
 Best Local Similarity 58.3%; Pred. No. 0.0037; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Db 133 EMRPSPTSLTKAVLYKRFNS 160

RESULT 4

Interleukin-6 receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

C:Accession: A17986
 F:102-171, 2001-2009, 1990
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gene
 A:Accession: A17986
 A:Accession: A17986; M01D:91060602
 A:Status: nucleic acid sequence not shown

A:Residues: 1-462 <SIG>
 A:Cross-references: GB:X51976; NID:953548; PIDN:CAA6238.1; PID:953549
 A:Superfamily: Cytokine receptor; receptor; cytokine receptor homology; immunog
 A:Keywords: cytokine receptor; receptor; status predicted <SIG>
 F:20-440/Product: Interleukin-6 receptor #status predicted <INT>
 F:40-94/Domain: Immunoglobulin homology <IM>
 F:117-306/Domain: Cytokine receptor homology <CR>
 F:358-385/Domain: transmembrane #status predicted <TR>
 F:386-462/Domain: intracellular #status predicted <INT>
 F:47-92/Disulfide bonds: #status predicted

Query Match 47.9%; Score 70; DB 1; Length 462;
 Best Local Similarity 54.2%; Pred. No. 0.008; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 129 EMRPSPTSLTKAVLYKRFNS 152

RESULT 5

Hypothetical protein XF202 [Imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82609
 F:102-171, 2001-2009, 1990
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gen
 A:Accession: D82609
 A:Accession: D82609; M01D:20365717
 A:Status: nucleic acid sequence not shown

A:Residues: 1-242 <SIG>
 A:Cross-references: GB:X51976; NID:949725; PIDN:CAA6237.1; PID:949726
 A:Experimental source: clone lambda 301
 A:Accession: J01015; M01D:90278354
 A:Title: Med. 171, 2001-2009, 1990
 A:Title: Functional, murine interleukin-6 receptor with the intracellular a particle gen
 A:Accession: J01015
 A:Accession: J01015; M01D:90278354
 A:Status: nucleic acid sequence not shown

Sequenzialpaarung

XX 22

Sequence 315 AA;
SQ

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Gencore version 4.5
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OM protein - protease search, using sw model

Run on: December 19, 2001, 16:13:35 ; Search time 170.68 Seconds
(without alignments)
5.208 Million cell updates/sec

Title: US-09-202-104A-1
Accession: 1 RYIIDGSLMLL 12

Scoring table: Biosum62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 08

Database: A_Geneseq_1101.*

1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	93.0	12	19	AAW52201	Interleukin-6 anca
2	53	93.0	16	16	AAR68954	Wild type Interleu
3	53	93.0	51	17	AAW00401	Interleukin-6 anca
4	53	93.0	151	17	AAR77393	Human mutant IL-6a
5	53	93.0	158	16	AAR77382	Human mutant IL-6a
6	53	93.0	162	16	AAR77381	Human mutant IL-6a
7	53	93.0	163	16	AAW00112	Human Interleukin-
8	53	93.0	163	17	AAW00112	Human IL-6 mutant
9	53	93.0	166	16	AAR77390	Human Interleukin-
10	53	93.0	167	17	AAR77649	Human IL-6 mutant
11	53	93.0	169	16	AAR77387	Human IL-6 mutant

12	53	93.0	173	16	AAR77389	Human IL-6 mutant
13	53	93.0	174	16	AAR75342	Hybrid human cytok
14	53	93.0	176	16	AAR75341	Hybrid human cytok
15	53	93.0	177	16	AAR77388	Human IL-6 mutant
16	53	93.0	181	16	AAR77387	Human IL-6 mutant
17	53	93.0	181	16	AAR77386	Human IL-6 mutant
18	53	93.0	181	16	AAR77385	Human IL-6 mutant
19	53	93.0	181	15	AAR77211	Human Interleukin-
20	53	93.0	181	17	AAW05586	-aa4a SSC muten o
21	53	93.0	182	16	AAR75346	Hybrid human cytok
22	53	93.0	183	15	AAR60125	Human Interleukin
23	53	93.0	184	9	AAP81158	Polypeptide with B
24	53	93.0	184	10	AAR94723	Sequence of variat
25	53	93.0	184	11	AAR05532	Human B-cell stim
26	53	93.0	184	11	AAR05532	Human B-cell stim
27	53	93.0	184	11	AAR03914	Polypeptide with h
28	53	93.0	184	11	AAR20783	Interleukin-6. A
29	53	93.0	184	15	AAR72129	Human Interleukin-
30	53	93.0	184	15	AAR51990	Mutant Interleukin
31	53	93.0	184	15	AAR52256	Interleukin 6. Ho
32	53	93.0	184	15	AAR75244	Hybrid human cytok
33	53	93.0	184	16	AAR66623	B-cell differentia
34	53	93.0	184	17	AAW02609	Interleukin-6. Ho
35	53	93.0	184	17	AAW02610	Interleukin-6 (O75
36	53	93.0	184	17	AAW02611	Interleukin-6 (O75
37	53	93.0	184	9	AAW02612	Polypeptide with B
38	53	93.0	185	9	AAP81159	Human B-cell diff
39	53	93.0	185	10	AAP81158	Synthetic Interleu
40	53	93.0	185	10	AAP81159	Synthetic Interleu
41	53	93.0	185	10	AAP81158	Segment of human B
42	53	93.0	185	11	AAW05275	Segment of human B
43	53	93.0	185	11	AAW05274	Segment of human B
44	53	93.0	185	11	AAW05275	Segment of human B
45	53	93.0	185	22	AAR73403	Human mature Inter

ALIGNMENTS

RESULT 1	AAW52201	standard; peptide; 12 AA.
ID	AAW52201	standard; peptide; 12 AA.
AC	AAW52201	
XX	09-JUN-1998	(first entry)
DE	Interleukin-6 antagonist peptide.	
KW	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;	
KM	acquired immune deficiency syndrome-related lymphoma; immune response;	
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;	
KM	Alzheimer's disease.	
XX	Synthetic.	
OS	Human sapiens.	
XX	NOV748728-A1.	
PN	24-DEC-1997.	
PD	19-JUN-1997; 97NO-RL00345.	
XX	20-JUN-1996; 96EP-0201720.	
PR	(KOST/) KOSTER H W.	
PA	Hoebie KRN, Van Leengoed LAMG;	
PT	WPI, 1998-063080/06.	
XX	New peptide(s) with Interleukin-6 agonist or antagonist activity -	
PT	useful for treatment, prevention and diagnosis of IL-6 associated	

Query Match 93.0%; Score 53; DB 17; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 RYLDGISALR 11
 |||||||
 DB 11 RYLDGISALR 21

RESULT 4

AA077393 standard; Protein: 151 AA.

AA077393:

17-APR-1996 (first entry)

Human mutant IL-6a/C3 (amino acids 5-19, 44-50 and 73-83 deleted).

Human Interleukin-6; IL-6a/C3 mutant; Increased stability;

amino acids 5-19, 44-50 and 73-83.

Homo sapiens.

JP07224097-A.

22-AUG-1995.

08-FEB-1994; 94JP-0014461.

08-FEB-1994; 94JP-0014461.

(ASAC) ASAH I GLASS CO LTD.

WPI: 1995-325556/42.

N-PSDB; AA094347.

Interleukin-6 mutant, related DNA and expression vectors - has

higher stability than natural Interleukin-6

Claim 1; Pages 15-16; 18pp; Japanese.

AA094348 encodes AA077393 the human IL-6 deletion mutant IL-6a/C3

which lacks the amino acids 5-19, 44-50 and 73-83

of the IL-6 type protein. The cDNA can be used for the recombinant prodn.

prodn. of IL-6a/C3 which has increased stability compared to wild

type IL-6.

Sequence 151 AA;

DB 15 RYLDGISALR 25

RESULT 5

AA077392 standard; Protein: 158 AA.

AA077392:

17-APR-1996 (first entry)

Human mutant IL-6a/C2 (amino acids 5-19 and 73-83 deleted).

Human Interleukin-6; IL-6a/C2 mutant; Increased stability;

recombinant; production; deletion mutant;

amino acids 5-19 and 73-83.

Homo sapiens.

Key Location/Qualifiers

mat_peptide 1..674

JP07224097-A.

22-AUG-1995.

08-FEB-1994; 94JP-0014461.

08-FEB-1994; 94JP-0014461.

(ASAC) ASAH I GLASS CO LTD.

WPI: 1995-325556/42.

N-PSDB; AA094347.

Interleukin-6 mutant, related DNA and expression vectors - has

higher stability than natural Interleukin-6

Claim 1; Pages 14-15; 18pp; Japanese.

AA094347 encodes AA077392 the human IL-6 deletion mutant IL-6a/C2

which lacks the amino acids 5-19, 44-50 and 73-83

of the IL-6 type protein. The cDNA can be used for the recombinant prodn.

prodn. of IL-6a/C2 which has increased stability compared to wild type

IL-6.

Sequence 158 AA;

DB 15 RYLDGISALR 25

RESULT 6

AA077391 standard; Protein: 162 AA.

AA077391:

17-APR-1996 (first entry)

Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).

Human Interleukin-6; IL-6a/C1 mutant; Increased stability;

recombinant; production; deletion mutant;

amino acids 5-19 and 44-50.

Homo sapiens.

JP07224097-A.

22-AUG-1995.

08-FEB-1994; 94JP-0014461.

08-FEB-1994; 94JP-0014461.

(ASAC) ASAH I GLASS CO LTD.

WPI: 1995-325556/42.

N-PSDB; AA094346.

Interleukin-6 mutant, related DNA and expression vectors - has higher stability than natural interleukin-6

Claim 1; Page 14; 18pp; Japanese.
AA094346 encodes AAR7391 the human IL-6 deletion mutant IL-6a'Cl, which lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the wild type protein. The cDNA can be used for the recombinant production of IL-6a'Cl, which has increased stability compared to wild type IL-6.

Sequence 162 AA:

Query Match 93.0%; Score 53; DB 16; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RYIDGISAIR 11
|||||
Db 15 rylldgsair 25

RESULT 7

AA000131 standard; Protein; 162 AA.

AA000131;

09-APR-1997 (first entry)

Human interleukin-6 fragment.

Secretory; signal peptide; P-factor; multicloning vector; PCR; animal protein; expression; production; recombinant; primer; fission yeast; human; serum albumin; interleukin-6; polymerase chain reaction; Schizosaccharomyces pombe; PO fragment.

Homo sapiens.

MO5623890-A1.

08-AUG-1996.

01-FEB-1996; 96WO-JP00198.

03-FEB-1995; 95JP-0017167.

(ASAC) ASAMI GLASS CO LTD.

Hama Y, Kumagai H, Nikaide K, Tohda H, Tsukamoto H;

WPI; 1996-371438/37.

Schizosaccharomyces pombe secretory signal peptide (P-factor) gene for production of vectors for expression of animal proteins in a fission yeast, pref. S. pombe, host

Example 4; Pages 28-29; 50pp; Japanese.
A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, a Schizosaccharomyces pombe secretory signal peptide fragment or P-factor fragment (PO fragment) DNA and preferably an animal cell viral promoter sequence and a neomycin resistance gene, can be used for the efficient production of a hIL-6 fragment, i.e. the present sequence, in a fission yeast host, preferably S. pombe, culture.

Sequence 162 AA:

Query Match 93.0%; Score 53; DB 17; Length 162;

Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RYIDGISAIR 11
|||||
Db 15 rylldgsair 25

RESULT 8

AA000132 standard; Protein; 163 AA.

AA000132;

09-APR-1997 (first entry)

Human interleukin-6 fragment.

Secretory; signal peptide; P-factor; multicloning vector; PCR; animal protein; expression; production; recombinant; primer; fission yeast; human; serum albumin; interleukin-6; polymerase chain reaction; Schizosaccharomyces pombe; PO fragment.

Homo sapiens.

MO5623890-A1.

08-AUG-1996.

01-FEB-1996; 96WO-JP00198.

03-FEB-1995; 95JP-0017167.

(ASAC) ASAMI GLASS CO LTD.

Hama Y, Kumagai H, Nikaide K, Tohda H, Tsukamoto H;

WPI; 1996-371438/37.

Schizosaccharomyces pombe secretory signal peptide (P-factor) gene for production of vectors for expression of animal proteins in a fission yeast, pref. S. pombe, host

Example 7; Pages 30-31; 50pp; Japanese.
A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, a Schizosaccharomyces pombe secretory signal peptide fragment or P-factor fragment (PI fragment) DNA and preferably an animal cell viral promoter sequence and a neomycin resistance gene, can be used for the efficient production of a hIL-6 fragment, i.e. the present sequence, in a fission yeast host, preferably S. pombe, culture.

Sequence 163 AA:

Query Match 93.0%; Score 53; DB 17; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RYIDGISAIR 11
|||||
Db 16 rylldgsair 26

RESULT 9

AA077390 standard; Protein; 166 AA.

AA077390;

17-APR-1996 (first entry)

XX	19-MAY-1994;	94US-0246427.
PR	(HUMA-) HUMAN GENOME SCI INC.	
PA	Adams MD, LI H, Ruben S;	
XX	WPI; 1996-020577/02.	
DR	N-PSDB; AAO8558.	
XX	Polynucleotide encoding interleukin 6-splice variant - used for	
PT	treating auto-immune diseases and inflammation.	
XX	Claim 1; Page 40; 54pp; English.	
CC	The human interleukin-6 splice variant (IL-6SV) AAR7649 is encoded	
CC	by AAO8558 (which is derived from an activated macrophage cDNA	
CC	library), and may be used in immunotherapeutic and	
CC	anti-inflammatory compounds, and for the treatment of patients	
CC	suffering from bone marrow transplant chemotherapy side effects,	
CC	corneal damage, and distal osteoarthritis, rheumatoid arthritis,	
CC	multiple myeloma, cardiac myxoma,	
CC	IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,	
CC	cervical cancer, rheumatoid arthritis and autoimmune diabetes),	
CC	and sepsis.	
XX		
SO	Sequence 167 AA;	
XX		
XX	Query Match 93.0%; Score 53; DA 17; Length 167;	
XX	Best Local Similarity 100.0%; Pred. No. 0.021;	
XX	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 RYLDGTSALR 11	
DB		
	31 RYLDGTSALR 41	
XX		
XX	RESULT 11	
XX	AAR7387	
ID	AAR7387 standard; Protein; 169 AA.	
XX		
AC	AAR7387;	
XX		
DE	17-APR-1996 (first entry)	
XX		
DE	Human IL-6 mutant IL-6a (amino acids 5-19 deleted).	
XX		
XX	Human interleukin-6; IL-6a mutant; Increased stability; 19,	
KW	recombinant; production; deletion mutant; amino acids 5-19,	
XX		
XX	Homo sapiens.	
XX		
XX	JP07224097-A.	
XX	22-AUG-1995.	
XX		
PD	08-FEB-1994; 94JP-0014461.	
XX		
PR	08-FEB-1994; 94JP-0014461.	
XX		
PA	(ASAC) ASAH1 GLASS CO LTD.	
XX		
DR	WPI; 1995-325566/42.	
XX	N-PSDB; AAO9342.	
XX		
PT	Interleukin-6 mutant, related DNA and expression vectors - has	
XX	higher stability than natural interleukin-6	
XX	Claim 1; Page 10; 16pp; Japanese.	
XX		
XX	AAO9342 encodes AAR7387 the human IL-6 deletion mutant IL-6a,	
XX	lacks the amino acids G1Y5-Leu19 of the wild type protein. The	

CC cDNA can be used for the recombinant prodn. of IL-6 α , which has
 XX increased stability compared to wild type IL-6.
 SQ Sequence 169 AA:

Query Match 93.0%; Score 53; DB 16; Length 169;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTIIDGISAIR 11
 |||
 Db 15 rylldglsair 25

RESULT 12
 AAR7389
 ID AAR7389 standard; Protein: 173 AA.
 AC AAR7389;
 XX 17-APR-1996 (first entry)
 DT Human IL-6 mutant IL-6C2 (amino acids 73-83 deleted).
 XX Human Interleukin-6; IL-6C2 mutant; increased stability;
 XX recombinant; production; deletion mutant; amino acids 73-83.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Key 1..319
 FE mapL-peptide /tag= a
 FN JP07224097-A.
 XX
 XX 22-AUG-1995.
 PD 08-FEB-1994; 94JP-0014461.
 PE 08-FEB-1994; 94JP-0014461.
 XX 08-FEB-1994; 94JP-0014461.
 PA (ASAC) ASAHI GLASS CO LTD.
 XX
 DR WPI: 1995-325556/42.
 N-PSDB: AAO94344.
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 XX higher stability than natural Interleukin-6
 PS Claim 1: Page 12: 18pp; Japanese.
 XX AAO94344 encodes AAR7389 the human IL-6 deletion mutant IL-6C2,
 CC which lacks the amino acids Cys73-Cys83 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
 CC has increased stability compared to wild type IL-6.
 SQ Sequence 173 AA:

Query Match 93.0%; Score 53; DB 16; Length 173;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTIIDGISAIR 11
 |||
 Db 30 rylldglsair 40

RESULT 13
 AAR75342
 ID AAR75342 standard; Protein: 174 AA.

AC AAR75342;
 XX 13-DEC-1995 (first entry)
 DT Hybrid human cytokine IIII.
 DE Hybrid cytokine; tumour proliferation; cancer therapy.
 XX
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 173 /note= "site of stop codon"
 XX
 XX W09513393-A.
 XX 18-MAY-1995.
 XX 07-NOV-1994; 94WO-US12873.
 XX 08-NOV-1993; 93US-0149101.
 XX (HUTC-) HUTCHINSON CANCER RES CENTER FRED.
 XX Leung DW, Todaro GJ;
 XX WPI: 1995-194111/25.
 N-PSDB: AAO87161.
 DR
 XX
 XX New hybrid cytokines with alpha helical sequences from different
 FT sources - also DNA encoding them, vectors and transformed cells,
 FT useful e.g. for treating cancer, remodelling bone etc.
 PS Claim 11: Page 31: 52pp; English.

CC The cytokine encoding genes for leukemia inhibitory factor (L),
 CC granulocyte-colony stimulating factor (G), interleukin-6 (I),
 CC interleukin-11 (E), ciliary neurotrophic factor (C) and
 CC oncostatin-M (O) have been cloned and reported in the literature.
 CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
 CC alpha-helical sequences of about 35-100 AAs. The invention
 CC provides a group of therapeutic hybrid cytokines, having a size ranging
 CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
 CC four alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
 CC upper case letters designate alpha-helical sequences, lower case
 CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
 CC the order of the alpha-helical sequences.
 CC sequences of IIII and IIL-alpha were derived from LIF. IIL-alpha has two
 CC fourth alpha-sequence was derived from LIF. IIL-alpha has two
 CC III and IV, as compared with IIII.
 SQ Sequence 174 AA:

Query Match 93.0%; Score 53; DB 16; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTIIDGISAIR 11
 |||
 Db 31 rylldglsair 41

RESULT 14
 AAR75341
 ID AAR75341 standard; Protein: 176 AA.
 XX
 XX AAR75341;
 XX 13-DEC-1995 (first entry)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:15:00 ; Search time 88.82 Seconds

Title: US-09-202-104A-1

Sequence: 1 RYIIDGISALRL 12

Scoring table: BIOSUM62

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	08
	Maximum Match	100%

Listing first 45 s

Database :

```
PIR_68: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *
```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	93	90	422	1	AA082	Interleukin-6 protein
2	90	87	420	2	AA082	Nucleoside transferase
3	87	84	410	3	AA082	Proteinase
4	41	71.9	386	2	EA8356	Proteinase
5	39	68.4	324	2	B86134	hypothetical protein
6	39	68.4	284	2	S56578	gamma protein - Escherichia coli
7	39	68.4	328	2	S18354	3-phosphoshikimate
8	39	68.4	316	2	XHP3YS	3-phosphoshikimate
9	39	68.4	516	2	XP03VS	3-phosphoshikimate
10	39	68.4	516	2	XP03VS	3-phosphoshikimate
11	38	66.7	468	4	7872	hypothetical protein
12	38	66.7	134	2	D27505	hypothetical protein
13	37	64.9	699	2	T13772	NADH dehydrogenase
14	37	64.9	136	2	E20735	hypothetical protein
15	37	64.9	334	2	EA83070	transferred hypothetical protein
16	36	63.2	633	2	C33053	paracetamol crystallase
17	36	63.2	199	2	T00218	type II secretion
18	36	63.2	199	2	T00218	hypothetical protein
19	36	63.2	289	2	E21933	hypothetical protein
20	36	63.2	402	2	E20850	DNA-directed DNA R
21	36	63.2	473	2	H83676	pyruvate dehydrogenase
22	36	63.2	783	2	T36811	Probable integral
23	36	63.2	483	1	JBDC22	DNA-directed DNA R
24	36	63.2	193	2	H83467	DNA polymerase III
25	35	61.4	192	2	EA8432	DNA polymerase III
26	35	61.4	192	2	S52429	response regulator
27	35	61.4	366	2	H83859	DNA polymerase III
28	35	61.4	377	2	H82122	DNA polymerase III
29	35	61.4	391	2	EA8393	aspartate aminotransferase

ALIGNMENTS

RESULT

interleukin-6 precursor [validated] - human

on factor

C:\Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000

R.; Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi, Y. *Macromolecules* 2000, 33, 1067.

A; Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g

A:Accession: A32648
A:Molecule type: DNA

A;Residues: 1-212 <YAS>

A./note: the authors translated the codon CAG for residue 130 as Gln
R:Zilberstein, A.; Budjeri, B.; Korn, J.H.; Revel, M.

A: Title: Structure and expression of cDNA and genes for

A;Accession: A25692

```
A;Residues: 1-212 <ZIL>
```

R; Hirano, T.; Yasukawa, Y.

Nature 324, 73-76, 1986.

A; Reference number: A93

A: molecule type: mRNA

A; Cross-references: GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850

Biochem. Biophys. Res. Commun. 163, 1056-1061 (1979).

A;Reference number: A33515

A:Residues: 1-212 <TON>

R;Haegeman, G.: Content

A;Title: Structural analysis of the sequence coding for an inducible 2

A;Accession: A25801

A; Residues: 1-212 <H1

A; Experimental source:

Query Match 66.7% **Score** 38. **Db 2:** Length 699;
Best Local Similarity 87.5%; **Pred.** No. 27;
Matches 7; **Conservative** 1; **Mismatches** 0; **Gaps** 0;

Oy	1 RYIDNGIS 8
Db	682 RYIDDCIS 689

RESULT 13
E70736
hydrophobic protein Ryv3408 - Mycobacterium tuberculosis (Strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70736
R:Title: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
Nadine, R.; Davies, K.; Devlin, K.; Felkewell, T.; Genoux, S.; Hamlin, N.; Holtroyd,
Patience 399, 537-544, 1998
A:Authors: Squares, R.; Solstun, J.E.; Taylor, K.; Whithead, S.; Barrett, B.G.
Affili: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MGIID: 98295987
A:Accession: E70736
A:Molecule type: nyc: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: L136 <COLD>

A:Cross-references: GB:z77165; GB:AL123456; NID:y93261609; PMID:CA001015.; PID:g1449379
A:Experimental source: GB:z77165; GB:AL123456; NID:y93261609; PMID:CA001015.; PID:g1449379

A:status: preliminary
A:sequence type: DNA
A:accession: 1587
R:Jomonan, M.P.; Dankoski, C.C.; Gilbert, M.F.; Garrow-Burke, M.C.; Groat, R.G.; Carr, R. Biol. Chem. 263, 561-567, 1988
A:field: Amino acid sequence and enzymoidal activity of the p2 crystal protein. Am. J.
A:reference number: A29193; MUID:88087146
A:sequence type: DNA
A:residues: 1587, 'FRY' <DON>
C:enclitics:
A:gene: cryBI

Query Match 64.98; Score 37; DB 2; Length 633;
Best Local Similarity 72.78; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YLISGISAALR 12
||| ||| |||
Db 306 YLISGISGWR 316

Search completed: December 19, 2001, 16:22:34
Job time: 454 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:16:45 : Search time 48.45 seconds
(without alignments)
9.081 Million cell updates/sec

Title: US-09-202-104a-1

Sequence: 1 RYIDIGISMLR 12

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36654827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	93.0	212	1 IL6_CERRO	P46550 cercocebus
2	53	93.0	212	1 IL6_HUMAN	P05231 homo sapien
3	53	93.0	212	1 IL6_MACCA	P79341 macaca fasc
4	53	93.0	212	1 IL6_MACCU	P51494 macaca msla
5	39	68.4	318	1 ARNO_TOBAC	P23281 nicotiana gl
6	39	68.4	318	1 ARNO_TOBAC	P23281 nicotiana gl
7	39	68.4	318	1 ARNO_PENNY	P11043 pennunia hyb
8	39	68.4	518	1 ARNO_TOBAC	P23981 nicotiana t
9	39	68.4	520	1 ARNO_LYCES	P10748 lycopersico
10	37	64.9	133	1 ARNO_MYCTU	P21253 bacillus th
11	37	64.9	633	1 C2AA_BACTO	P05079 mycobacteri
12	36	63.2	782	1 DP38_MYCTU	P41323 conis famli
13	36	63.2	782	1 DP38_MYCTU	P41323 conis famli
14	35	61.4	207	1 IL6_CANPA	P28819 phoca vitul
15	35	61.4	209	1 IL6_PPROV	P72856 streptomyc
16	35	61.4	391	1 DP38_STYV3	P65701 mycobacteri
17	35	61.4	454	1 IL6_MYCTU	P31545 streptomyc
18	35	61.4	475	1 WMR_STROO	P18182 streptococ
19	35	61.4	790	1 TDBA_ECOLI	P20857 anabaena sp
20	34	59.6	410	1 VYD1_CNSP	P20857 anabaena sp
21	34	59.6	410	1 VYD1_CNSP	P20857 anabaena sp
22	34	59.6	454	1 PYRC_METHI	P17688 brassica na
23	34	59.6	516	1 ARNO_BRANA	P05466 arabidopsis
24	34	59.6	520	1 ARNO_ARATH	P04633 mus musculu
25	34	59.6	681	1 TBRL_MOUSE	P01650 homo sapien
26	34	59.6	682	1 TBRL_HUMAN	P09585 homo sapien
27	34	59.6	723	1 TBRL_HUMAN	P09585 homo sapien
28	34	59.6	723	1 TBRL_HUMAN	P09585 homo sapien
29	34	59.6	1830	1 B2E6_ARX5	P05466 arabidopsis
30	33	57.9	188	1 SPR_ECOLI	P77688 brassica na
31	33	57.9	205	1 IL6_MYCOC	P28819 phoca vitul
32	33	57.9	212	1 IL6_PIG	P28819 phoca vitul
33	33	57.9	282	1 ARDE_METUA	P26893 sus scrofa
					P58484 methanococ

ALIGNMENTS

RESULT	ID	STANDARD	PRT	212 AA.
1	IL6_CERRO			
2	IL6_HUMAN			
3	IL6_MACCA			
4	IL6_MACCU			
5	ARNO_TOBAC			
6	ARNO_TOBAC			
7	ARNO_PENNY			
8	ARNO_TOBAC			
9	ARNO_LYCES			
10	ARNO_MYCTU			
11	C2AA_BACTO			
12	DP38_MYCTU			
13	DP38_MYCTU			
14	IL6_CANPA			
15	IL6_PPROV			
16	DP38_STYV3			
17	IL6_MYCTU			
18	WMR_STROO			
19	TDBA_ECOLI			
20	VYD1_CNSP			
21	VYD1_CNSP			
22	PYRC_METHI			
23	ARNO_BRANA			
24	ARNO_ARATH			
25	TBRL_MOUSE			
26	TBRL_HUMAN			
27	TBRL_HUMAN			
28	B2E6_ARX5			
29	SPR_ECOLI			
30	IL6_MYCOC			
31	IL6_PIG			
32	ARDE_METUA			
33	ARDE_METUA			

Query Match 93.08; Score 53; DB 1; Length 212;
 Best Local Similarity 100.0%; Pctd. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 RYILDISALR 11
 |||||
 Db 58 RYILDISALR 68

RESULT 2
 LOC. HUMAN STANDARD: PRT: 212 AA.
 AC P05231.
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last annotation update)
 DE 10-NOV-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERLEUKIN-6) (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERLEUKIN-6) (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 OS Homo sapiens (human).
 OS Homo sapiens (human).
 OS Homo sapiens (human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI:TaxID=9606.
 RN [1]
 RS SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA HILANO T., YASUKAWA K., HARADA H., TAGA T., MATSUNO Y., MATSUDA T.,
 RA KASHIWAMURA S.-I., NAKAJIMA K., KOYAMA K., IWANAGISAWA A., TSUNASHIMA S.,
 RA SAKIYAMA F., MATSUI H., TAKAHARA Y., TANIGUCHI T., KISHIMOTO T.;
 RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
 B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-87063433; PubMed-3500852.
 RA YASUKAWA K., HILANO T., MATSUNO Y., MURATANI K., MATSUDA T.,
 RA NAKAJIMA K., KISHIMOTO T.;
 RT "Structure and expression of human B cell stimulatory factor-2
 (BSF-2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-87067433; PubMed-3538015.
 RA MAY L.T., HELFICOTT D.C., SENIGAL P.B.;
 RT "Anti-beta-2-interferon antibodies inhibit the increased expression of
 HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 structural studies of the beta-2 interferon involved.";
 RL J. Natl. Acad. Sci. U.S.A. 83:6957-6961(1986).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-8705318; PubMed-3023045.
 RA ZILBERTSTEIN A., RUGGIERI R., KOHN J.H., REVEL M.;
 RT "Structure and expression of cDNA and genes for human
 interferon-beta-2, a distinct species inducible by growth-stimulatory
 cytokines.";
 RL EMBO J. 3:2529-2537(1986).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-8808768; PubMed-3320204;
 RA BRAKENHOFF J.P.J., DE GROOT E.R., EVERS R.F., PANNEKOOK H.,
 RA AARLEN L.A.;
 RT "Molecular cloning and expression of hybridoma growth factor in
 (6) immunol. 139:4116-4121(1987).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-8931958; PubMed-2789533;
 RA TONOUCHI N., MIWA K., KARASUYAMA H., MATSUI H.;
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 stabilization of the mRNA and high-level expression in mouse NIH3T3
 cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RU
 RA SEQUENCE FROM N.A.
 RA TISSUE-Ribblast.
 RA MEDLINE-87004683; PubMed-3758081;
 RA HEGEMAN G., CONTENT J., VOLCHART G., DEYNCK R., TAVERNIER J.,
 RA PIERS M.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-89193317; PubMed-3266463;
 RA WONG G., WILEK-GIAMOCITI J., HEWICK R., CLARK S., OGAWA M.;
 RT "Interleukin 6: identification as a hematopoietic colony-stimulating
 factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RU
 RA SEQUENCE FROM N.A.
 RA MEDLINE-93178270; PubMed-1291290;
 RA CHEN Q.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 mammalian cells after gene transfer.";
 RL Chung-Hua Chung Hua Tsa Chih 14:340-344(1992).
 RU
 RA SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RA VAN DAMME J., VAN BEEUNEN J., DECOCK B., VAN SNIJCK J., DE LEY M.,
 RA BILLIAU A.;
 RT "Separation and comparison of two monokines with
 lymphocyte-activating factor activity: IL-1-beta and hybridoma growth
 factor (hGF). Identification of leukocyte-derived hGF as IL-6.";
 RL J. Immunol. 140:1536-1541(1988).
 RU
 RA SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RA BILLOTTO R., LA FLORA A., BERTOLERO F., ORSINI G., VALASSINA B.,
 RA ZILBERTSTEIN A., DE FILIPPI V., POLVERIO F., FONTANA A.;
 RT "Structure, stability and biological properties of a recombinant
 truncated form of recombinant human interleukin-6 containing a single
 disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RU
 RA DISULFIDE BONDS.
 RA MEDLINE-89286115; PubMed-2472117;
 RA OLSON C.L., BOONE T.C., CRANDALL B.C., MENDIAZ E.A., LU H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 human interleukin-1.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RU
 RA MOTAGENESIS.
 RA MEDLINE-91243808; PubMed-2037043;
 RA LAETICKEN C., KRUETZIGER A., MOELLER C., BEHNICH P.C., ROSE-JOHN S.;
 RT "Evidence for the importance of a positive charge and an
 alpha-helical structure of the C-terminus for biological activity of
 PHS Lett. 262:265-267(1991).
 RU
 RA STRUCTURE BY NMR.
 RA MEDLINE-96134845; PubMed-8555185;
 RA NISHIMURA K., MATSUDA H., GONDA H., SHIMADA I., ARATA Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 by NMR spectroscopy.";
 RL J. Biomol. NMR 10:261-268(1996).
 RU
 RA STRUCTURE BY NMR.
 RA MEDLINE-97303053; PubMed-9159484;
 RA XU G.-Y., YU H.-A., HONG J., STAHL M., McDONAGH T., KAY L.E.,
 RA CUNNINGHAM D.A.;
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RU
 RA X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE-97224126; PubMed-9118960;


```

CC      or send an email to license@lsb-sib.ch).
CC
CC      EMBL, M21084, AAA35699.1; -.
DR      PIR, A28196; XMPVS.
DR      InterPro: IPR001966; EPSP_synthase.
DR      PIR, A28196; XMPVS.
DR      Prodom: P0001667; EPSP_synthase.
DR      PROSITE, PS00104; EPSP_SYNTHASE.1.
DR      PROSITE, PS00885; EPSP_SYNTHASE.2.1.
KW      Aromatic amino acid biosynthesists; Transferase; Translt peptid;
KW      Chloroplast; Herbicide resistance.
FT      TRANSIT
FT      CHAIN
FT      73
FT      72
FT      56
FT      3-PROSPOSHIKIMATE.1-
FT      3-PROSPOSHIKIMATE.2-
FT      1A75E1EB7E7A98 C8C64;
FO      SEQUENCE 516 AA: 55537 MW: 1A75E1EB7E7A98 C8C64;

Cy      1 PYRIDOSIMR 11
Db      191 RYLVDSVPRRR 201

Query Match      68.4%; Score 39; DB 1; Length 516;
Best local Similarity 54.5%; Pred. No. 5.3;
Matches      3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
AR01.TOBAC
ID      AR01.TOBAC
STANDARD:
PRT: 518 AA.

01-MAR-1993 (Rel. 21, Created)
01-MAR-1993 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3-PROSPOSHIKIMATE.1-CARBOXYVINYLTANSFERASE.1 [EC 2.5.1.19]
3-ENOLPYRUVYLSHIKIMATE-3-PROSPHATE SYNTHASE 1) (EPSP SYNTHASE 1).
EPSPS-1.
Nicotiana tabacum (Common tobacco)
Solanum tuberosum (Potato)
Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots;
Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;

SEQUENCE FROM N.A.
MEDLINE-9203779; PubMed-1932690;
Ward R., Jones J., Kellier S., Goldstrong P.B.:
cDNA cloning and characterization of the tobacco
enolpyruvylshikimate-3-phosphate synthase in glyphosate-tolerant
tobacco cells *;
Plant Mol. Biol. 17:1137-1138(1991).
-1- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PROSPOSHIKIMATE =
ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYLT)-3-PROSPOSHIKIMATE.
PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHOLICACIDE WITHIN
THE BIOSYNTHESIS OF AN ANTIMIC BIANO ACIDS (THE SHIKIMATE PATHWAY).
-1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF THE POTENT,
BROAD-SPECTRUM HERBICIDE, GLYPHOSATE [N-(PHOSPHONOMETYL)GLYCINE].
OVERPRODUCTION OF EPSP LEADS TO GLYPHOSATE TOLERANCE.
-1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.

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or send an email to license@lsb-sib.ch).
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FT CONFLICT 739 782 LDYORSPDYEHYHNRLODPVAGCILLPEIDENFATL
 FT SEQUENCE 782 AA: 89921 MW: 286840412ACR45A1 CRC64:
 50

Query Match
 Best Local Similarity 63.2%; Score 36; DB 1; Length 782;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDIGISLR 11
 DB 271 RYLDIGISLR 281

RESULT 14

ID IL6_CANFA STANDARD; PRT; 207 AA.

AC 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DE 15-JUL-1998 (rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).

IL6.
 Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI_TaxID=9615;

SEQUENCE FROM N.A.

RE STRAIN-WONGSEL; Pubmed-7913298;

RA MEDLINE-94303924; PubMed-7913298;
 RA Mukelka G. L., Youker K. A., Hawkins H. X., Pettard J. L.,
 RA Regulation of ICM-1 and IL-6 in myocardial ischemia: effect of

RT Am. N.Y. Acad. Sci. 723:258-270(1994).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC REPRODUCTION IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY

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CC - send email to license@isb-sib.ch).

CC EMBL: 012234; AA083030.1; -

DR HSP: P05231; 21L6.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSF.

DR PRODOM: PD004356; Interleukin_6; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

DR CYTOKINE; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 POTENTIAL.

FT CHAIN 7 207 INTERLEUKIN-6.

FT DISULFID 67 103 BY SIMILARITY.

FT FT 96 103 BY SIMILARITY.

SEQUENCE 207 AA; 22945 MW; 455401948AAC0F50 CRC64;

OY 1 RYLDIGISLR 11
 DB 53 RYLDIGISLR 63

RESULT 15

ID IL6_PROVI STANDARD; PRT; 209 AA.

AC 028819; 2000 (rel. 39, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)

DE 30-MAY-2000 (rel. 39, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6) (TRANSMIT)

IL6.
 Phoca vitulina (Harbor seal).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Phocidae; Phoca.

NCBI_TaxID=9770;

SEQUENCE FROM N.A.

RE MEDLINE-96163018; PubMed-8575817;

RA King D. P., Schrenzel M. D., McKnight M. L., Reitarson T. H., Hanni K. D.,

RA Molecular cloning and sequencing of interleukin 6 cDNA fragments from

RT the harbor seal (Phoca vitulina). Killer whale (Orcinus orca), and

RT Southern sea otter (Enhydra lutris nereis).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC REPRODUCTION IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC - send email to license@isb-sib.ch).

DR EMBL: I46802; AB01430.1; -

DR HSP: P05231; 21L6.

DR InterPro: IPR003574; Interleukin_6.

DR Pfam: PF00489; IL6; 1.

DR SMART: SM00126; IL6; 1.

DR CYTOKINE; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 POTENTIAL.

FT CHAIN 27 209 INTERLEUKIN-6.

FT DISULFID 69 75 BY SIMILARITY.

FT FT 98 108 BY SIMILARITY.

SEQUENCE 209 AA; 23483 MW; 75144922843B48E9 CRC64;

Query Match
 Best Local Similarity 61.4%; Score 35; DB 1; Length 209;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDIGISLR 11
 DB 55 RYLDIGISLR 65

Search completed: December 19, 2001, 16:26:13
 Job time: 568 sec

GenCode version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:16:15

(Search time 157.32 Seconds
(without alignments)
11.157 Million cell updates/sec)

Title: US-09-202-104a-1
Sequence: 1 RYIDDISAARL 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 segs, 14672329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database:

1: SP:archae:17.*
2: SP:bacteria:.*
3: SP:fungi:.*
4: SP:human:.*
5: SP:invertebrate:.*
6: SP:mammal:.*
7: SP:metazoa:1483
8: SP:protist:.*
9: SP:protist:.*
10: SP:plant:.*
11: SP:rodent:.*
12: SP:virus:.*
13: SP:vertebrate:.*
14: SP:unclassified:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.0	209	6	097540	097540 actus nancy
2	49	175	6	097TH4	097TH4 actus nancy
3	49	175	6	097TH4	097TH4 actus nancy
4	46.0	209	6	097TH4	097TH4 actus nancy
5	46.0	209	6	097TH4	097TH4 actus nancy
6	42	175	6	097TH4	097TH4 actus nancy
7	42	175	6	097TH4	097TH4 actus nancy
8	42	175	6	097TH4	097TH4 actus nancy
9	39	175	6	097TH4	097TH4 actus nancy
10	39	175	6	097TH4	097TH4 actus nancy
11	39	175	6	097TH4	097TH4 actus nancy
12	38	175	6	097TH4	097TH4 actus nancy
13	38	175	6	097TH4	097TH4 actus nancy
14	38	175	6	097TH4	097TH4 actus nancy
15	38	175	6	097TH4	097TH4 actus nancy
16	37	175	6	097TH4	097TH4 actus nancy
17	37	175	6	097TH4	097TH4 actus nancy
18	37	175	6	097TH4	097TH4 actus nancy
19	37	175	6	097TH4	097TH4 actus nancy

20	37	64.9	633	2	0956N4	0956N4 bacillus th
21	36	63.2	199	2	032572	032572 escherichia
22	36	63.2	288	2	025656	025656 helicobacter
23	36	63.2	288	2	025656	025656 helicobacter
24	36	63.2	288	2	025656	025656 helicobacter
25	36	63.2	402	2	09BNV6	09BNV6 bacillus th
26	36	63.2	473	2	09K936	09K936 bacillus th
27	36	63.2	483	2	09S242	09S242 streptomyces
28	36	63.2	774	2	09E175	09E175 pseudomonas
29	36	63.2	1371	2	09RBS8	09RBS8 xyloella fas
30	36	63.2	1371	2	09RBS8	09RBS8 xyloella fas
31	35	61.4	139	2	09RBS9	09RBS9 micrococcus
32	35	61.4	183	2	09K253	09K253 gramia citr
33	35	61.4	192	2	0912V7	0912V7 pseudomonas
34	35	61.4	194	1	09H204	09H204 thermoplasma
35	35	61.4	207	6	09H204	09H204 thermoplasma
36	35	61.4	323	2	09H204	09H204 thermoplasma
37	35	61.4	366	2	09H204	09H204 thermoplasma
38	35	61.4	376	10	09FRK7	09FRK7 arabidopsis
39	35	61.4	381	2	09H206	09H206 vibrio chol
40	35	61.4	638	2	09H202	09H202 pseudomonas
41	35	61.4	813	2	09H202	09H202 pseudomonas
42	35	61.4	841	2	09H202	09H202 pseudomonas
43	35	61.4	1135	2	09H202	09H202 pseudomonas
44	35	61.4	1436	2	09H202	09H202 pseudomonas
45	35	61.4	1436	2	09H202	09H202 pseudomonas

ALIGNMENTS

RESULT 1

097540 PRELIMINARY: PRT: 209 AA.

AC 097540: (PREDICTED: 10. Created)

DT 01-MAY-1999 (PREDICTED: 10. Last sequence update)

DT 01-JUN-2003 (PREDICTED: 11. Last annotation update)

DE INTERLEUKIN-6 (FRAGMENT).

GN IL-6.

OS Actus nancyense (owl monkey).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.

OX NCBI_taxonomy=37293;

RA SEQUENCE FROM N.A.

RA Scheperry S.J., Hernandez E., Moreno A., Patariroyo M.E., Murillo L.A.;

RA "Identification, cloning and sequencing of different interleukin genes

in 4 Actus species."

RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF014510; A001536.1; .

DR HSSP: P05231; 1ALU.

DR PIR: P00048; 1IL6.1; IL6.MCF.GCSP.

DR PRINTS: P00043; IL6GSPSP.

DR SMART: SM00126; IL6.1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

FT NON_TER 1

FT SEQUENCE 209 AA: 23406 MW: 844F085D084002DD CRC64;

Query Match 93.0%; Score 53; DB 6; Length 209;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 0; Indels 0;

DB 58 RYIDDISAARL 68

097TH4

097TH4

097TH4

097TH4

097TH4

097TH4

097TH4

097TH4

ID	G9TH4	PRELIMINARY	PRT: 175 AA.
DT	01-MAY-2000 (TRENBERG)	13, Created	
DL	01-MAY-2000 (TRENBERG)	11, Last sequence update	
DT	01-JUN-2001 (TRENBERG)	17, Last annotation update	
DE	INTERLEUKIN-6 (FRAGMENT).		
GN	IL-6.		
OS	Actus nigricans (black-headed night monkey).		
OC	Eukaryota; Metazoa; Chordata; Cnidaria; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.		
OC	NCBI_TaxId=91753.		
RP	SEQUENCE FROM N.A.		
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,		
RA	Patarroyo M.E.;		
RA	*Actus nigricans gene for IL-6.*		
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AF097322; AAC21297.1; -		
DR	HSSP: P05231; IAUU		
DR	PIR: P05231; IAUU		
DR	PIR: P05231; IAUU		
DR	Pfam: PF00489; IL6; 1		
DR	PRINTS: PR00433; IL6CSFNGF.		
DR	SMART: SM00126; IL6; 1.		
DR	PROSITE: PS00254; INTERLEUKIN-6; 1.		
DR	NON_TER	1	
FT	SEQUENCE	175 AA: 28CC57ACB99A199 CRC64;	
SQ			
Query Match			
	Best local similarity	90.9%	Pred. No. 0.15;
	Matches	10: Conservative	1; Mismatches 0; Indels 0; Gaps 0;
QY	1 RYLDIGISAIR 11		
DB	58 RYLDIGISAIR 68		
DT	01-MAY-2000 (TRENBERG)	13, Created	
DL	01-MAY-2000 (TRENBERG)	11, Last sequence update	
DT	01-JUN-2001 (TRENBERG)	17, Last annotation update	
DE	INTERLEUKIN-6 (FRAGMENT).		
GN	IL-6.		
OS	Actus lemurinus (Northern gray-necked night monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.		
OC	NCBI_TaxId=94317.		
RP	SEQUENCE FROM N.A.		
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,		
RA	Patarroyo M.E.;		
RA	*Actus lemurinus gene for IL-6.*		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AF097323; AAC21298.1; -		
DR	HSSP: P05231; IAUU		
DR	PIR: P05231; IAUU		
DR	PIR: P05231; IAUU		
DR	Pfam: PF00489; IL6; 1		
DR	PRINTS: PR00433; IL6CSFNGF.		
DR	SMART: SM00126; IL6; 1.		
DR	PROSITE: PS00254; INTERLEUKIN-6; 1.		
DR	NON_TER	1	
FT	SEQUENCE	209 AA: 23115 NW: A0A3DFAA4BF550CC CRC64;	
SQ			
Query Match			
	Best local similarity	90.9%	Pred. No. 0.18;
	Matches	10: Conservative	1; Mismatches 0; Indels 0; Gaps 0;
QY	1 RYLDIGISAIR 11		

[illegible]

LA Umlstead R.G., Reeves P.A.;
 RL Ann. Mo. Bot. Gard. 82:176-193(1995).
 CC -1- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
 CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CC CHAINS.

Job time: 543 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: December 19, 2001, 16:14:15
(without alignments)
3.439 Million cell updates/sec

Title: US-09-202-104a-1

Sequence: 1 RYLDIGISLARL 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:*

- 1: /cgn2.6/prodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2.6/prodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2.6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2.6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2.6/prodata/2/1aa/PCNUS.COMB.pep:*
- 6: /cgn2.6/prodata/2/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	93.0	12	2	US-08-591-438-17
2	53	93.0	16	1	US-08-567-047-9
3	53	93.0	16	2	US-08-567-048-9
4	53	93.0	162	2	US-08-716-317-10
5	53	93.0	163	2	US-08-318-317-15
6	53	93.0	164	1	US-08-318-193-60
7	53	93.0	167	1	US-08-246-427-5
8	53	93.0	167	5	US-08-567-0609-2
9	53	93.0	167	5	US-08-567-0609-2
10	53	93.0	172	4	US-08-149-101A-21
11	53	93.0	172	5	US-08-149-101A-21
12	53	93.0	174	4	US-08-149-101A-20
13	53	93.0	174	5	US-08-149-101A-20
14	53	93.0	181	1	US-08-209-182C-4
15	53	93.0	181	1	US-08-209-182C-4
16	53	93.0	182	4	US-08-149-101A-25
17	53	93.0	182	5	US-08-149-101A-25
18	53	93.0	183	1	US-08-009-973-1
19	53	93.0	184	1	US-08-567-047-2
20	53	93.0	184	2	US-08-567-047-2
21	53	93.0	184	2	US-08-567-048-2
22	53	93.0	184	2	US-08-567-048-2
23	53	93.0	184	2	US-08-567-048-2
24	53	93.0	184	4	US-08-149-101A-22
25	53	93.0	184	4	US-08-149-101A-22
26	53	93.0	184	5	US-08-149-101A-22
27	53	93.0	184	5	US-08-149-101A-22

28	53	93.0	184	5	PCT-US94-12873-23	Sequence 23, Appl
29	53	93.0	185	1	US-07-632-070B-1	Patent No. 5186931
30	53	93.0	185	1	US-07-632-070B-1	Sequence 1, Appl1
31	53	93.0	185	1	US-07-618-181A-2	Sequence 4, Appl1
32	53	93.0	185	1	US-07-618-181A-2	Sequence 4, Appl1
33	53	93.0	185	1	US-07-618-181A-6	Sequence 6, Appl1
34	53	93.0	185	1	US-07-618-181A-8	Sequence 8, Appl1
35	53	93.0	185	1	US-08-231-575-2	Sequence 2, Appl1
36	53	93.0	185	1	US-08-231-575-4	Sequence 4, Appl1
37	53	93.0	185	1	US-08-231-575-6	Sequence 6, Appl1
38	53	93.0	185	1	US-08-231-575-8	Sequence 8, Appl1
39	53	93.0	185	1	US-08-246-427A-5	Sequence 5, Appl1
40	53	93.0	185	1	US-08-246-427A-5	Sequence 5, Appl1
41	53	93.0	185	2	US-08-765-630-5	Sequence 2, Appl1
42	53	93.0	185	5	PCT-US93-06928-2	Sequence 2, Appl1
43	53	93.0	185	5	PCT-US93-06928-2	Sequence 2, Appl1
44	53	93.0	185	5	PCT-US93-06928-4	Sequence 4, Appl1
45	53	93.0	185	5	PCT-US93-06928-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-591-438-17
? Sequence 17, Application US/08591438
? Patent No. 5939063
? GENERAL INFORMATION:
? INVENTOR: Scully, Scott, Murphy & Presser
? APPLICANT: Shannon, Mary F.
? TITLE OF INVENTION: HAEMOLETIC GROWTH FACTOR ANTAGONISTS
? NUMBER OF SEQUENCES: 47
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Scully, Scott, Murphy & Presser
? STREET: 400 Garden City Plaza
? STATE: Garden City
? COUNTRY: New York
? ZIP: 11530
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE STATEMENT: Release #1.0, Version #1.30
? CURRENCY: US/08/591,438
? FILING DATE: 08-APR-1996
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Disigilio Esq., Frank S.
? REGISTRATION NUMBER: 31,346
? EXPIRATION/DOCKET NUMBER: 91912
? TELEPHONE: (516) 742-4343
? TELEFAX: (516) 742-4366
? INFO: 230 901 SANS UR
? INFORMATION FOR SEQ ID NO: 17:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 12 amino acids
? STRANDNESS: acd
? TOPOLOGY: linear
? MOLECULE TYPE: polypeptide
US-08-591-438-17

Query Match: 93.0% Score 53 DB 2 Length 12
Sequence Similarity: 100.0% Pct-Mismatches: 0.00014
Matches 11 Conservative 0 Mismatches 0 Indels 0 Gaps 0
|||||||

Db 1 RYLDIGISALR 11

RESULT 2
US-08-567-047-9
; Sequence 9, Application US/08567047
; Patent No. 5789552
; Patent No. 5789552 5789555
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: CLIBERTO, Genaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,047
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; PRIORITY NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; TELEPHONE: 202-628-5197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: no
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria as recombinant protein
; FEATURE:
; NAME/KEY: wild type interleukin-6
; IDENTIFICATION METHOD: polyclonal gel
; OTHER INFORMATION: sequence of wild type of interleukin 6,
; OTHER INFORMATION: from position 27 to position 42
US-08-567-047-9

Query Match 93.0%; Score 53; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDIGISALR 11
DB 4 RYLDIGISALR 14

RESULT 3

US-08-567-048-9

; Sequence 9, Application US/08567048
; Patent No. 5801998
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAH, Armin
; TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,048
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; TELEPHONE: 202-628-5197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-737-3528
; TELEFAX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: no
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria as recombinant protein
; FEATURE:
; NAME/KEY: wild type interleukin-6
; IDENTIFICATION METHOD: polyclonal gel
; OTHER INFORMATION: sequence of wild type of interleukin 6,
; OTHER INFORMATION: from position 27 to position 42
US-08-567-048-9

Query Match 93.0%; Score 53; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDIGISALR 11
DB 4 RYLDIGISALR 14

RESULT 4
US-08-716-317-10
; Sequence 10, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: YUKO

```

1 APPLICANT: TOHDA, HIDEKI
2 APPLICANT: TSURUMOTO, HIROKO
3 APPLICANT: MIKAIJO, KIYOKAZU
4 APPLICANT: KIKUCHI, HIROAKI
5 TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
6 TITLE OF INVENTION: VECTOR CONTAINING IT
7 NUMBER OF SEQUENCES: 35
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
10 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
11 STATE: ARLINGTON
12 COUNTRY: USA
13 ZIP: 22202
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA: US/08/716.317
19 FILING DATE: 02-OCT-1996
20 CLASSIFICATION: 435
21 PRIOR APPLICATION NUMBER: PCT/JP96/00198
22 FILING DATE: 01-FEB-1996
23 PRIOR APPLICATION DATA: JP 17167/1995
24 FILING DATE: 03-FEB-1996
25 ATTORNEY/AGENT INFORMATION:
26 NAME: OBLON, NORMAN F.
27 REGISTRATION NUMBER: 24,618
28 REFERENCE/DOCKET NUMBER: 59-924-0 PCT
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 703-413-3000
31 TELEFAX: 703-413-2220
32 INFORMATION FOR SEQ ID NO: 10:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 162 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: protein
39 US-08-716-317-10

```

```

Query Match          93.0%; Score 53; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 RYLDGTSALR 11
    |||||
DB 15 RYLDGTSALR 25

```

```

RESULT 5
US-08-716-317-15
1 Sequence 15, Application US/08716317
2 Sequence 15, Application US/08716317
3 GENERAL INFORMATION:
4 APPLICANT: HAMA, YUKO
5 APPLICANT: TOHDA, HIDEKI
6 APPLICANT: TSURUMOTO, HIROKO
7 APPLICANT: MIKAIJO, KIYOKAZU
8 APPLICANT: KIKUCHI, HIROAKI
9 TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
10 TITLE OF INVENTION: VECTOR CONTAINING IT
11 NUMBER OF SEQUENCES: 35
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
14 ADDRESSEE: P.C.
15 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

```

```

1 CITY: ARLINGTON
2 STATE: VA
3 COUNTRY: USA
4 ZIP: 22202
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: PatentIn Release #1.0, Version #1.30
9 CURRENT APPLICATION DATA: US/08/716.317
10 FILING DATE: 02-OCT-1996
11 CLASSIFICATION: 435
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: PCT/JP96/00198
14 FILING DATE: 01-FEB-1996
15 PRIOR APPLICATION DATA: JP 17167/1995
16 FILING DATE: 03-FEB-1996
17 ATTORNEY/AGENT INFORMATION:
18 REFERENCE/DOCKET NUMBER: 59-924-0 PCT
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 703-413-3000
21 TELEFAX: 703-413-2220
22 INFORMATION FOR SEQ ID NO: 15:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 163 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: peptide
29 US-08-716-317-15

```

```

Query Match          93.0%; Score 53; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 RYLDGTSALR 11
    |||||
DB 16 RYLDGTSALR 26

```

```

RESULT 6
US-08-318-193-60
1 Sequence 60, Application US/08318193
2 Patent No. 564163
3 GENERAL INFORMATION:
4 APPLICANT: GARYIN, ROBERT T.
5 APPLICANT: KATZ, LAWRENCE S.
6 TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION SYSTEM FOR THE SECRETION
7 TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
8 TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
9 NUMBER OF SEQUENCES: 91
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Foley & Lardner
12 STREET: 1600 Lagonal Road, Suite 500
13 CITY: Alexandria
14 STATE: Virginia
15 COUNTRY: USA
16 ZIP: 22313-0299
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA: US/08/318.193
22 FILING DATE:
23 CLASSIFICATION: 435

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,314
 FILING DATE: MAY 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 18740/116 CACO
 TELEPHONE: (703)956-0300
 TELEFAX: (703)963-4109
 FILING DATE: MAY 18, 1994
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-316-193-60

Query Match 93.0%: Score 53; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYLDGSLALR 11
 DB 10 RYLDGSLALR 20

RESULT 7
 US-08-246-427A-2
 Sequence 2, Application US/08246427A
 Filing Date: MAY 18, 1994
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice Variant
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: CABELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESS: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 OPERATING SYSTEM: IBM PS/2
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,427A
 FILING DATE: Submitted herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 18, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS: 2:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN

US-08-246-427A-2

Query Match 93.0%: Score 53; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYLDGSLALR 11
 DB 31 RYLDGSLALR 41

RESULT 8
 US-08-766-620-2
 Sequence 2, Application US/08766620
 Patent No. 5958400
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice Variant
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: CABELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 OPERATING SYSTEM: IBM PS/2
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,620
 FILING DATE: December 12, 1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 18, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-593 (PPI20)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS: 2:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-766-620-2

Query Match 93.0%: Score 53; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYLDGSLALR 11
 DB 31 RYLDGSLALR 41

RESULT 9
 PCT-US95-06094-2
 Sequence 2, Application PC/TUS9506094
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice Variant

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: CARELLA, BYRNE, BAIN, GIUFFILIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
CITY: NEW JERSEY
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION NUMBER: PCT/US95/06094
FILING DATE: Submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDNESS:
TOPOLOGY: LINEAR
MOLECULAR TYPE: PROTEIN
PCT-US95-06094-2
Query Match 93.0%; Score 53; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISLR 11
DB 31 RYLDGISLR 41
RESULT 10
US-08-149-101A-21
Sequence 21 Application US/08149101A
Patent No. 6171824
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Leung, David W.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Cell Therapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE, 1.44Mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,101A
FILING DATE: 8-No. 6171824-1993

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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/097,869
FILING DATE: 27-Jul-1993
ATTORNEY/AGENT INFORMATION:
NAME/AGENT: INGHAM, B.N. and Faciszewski, Stephen
REGISTRATION NUMBER: 32,585 and 36,131, respectively
REFERENCE/DOCKET NUMBER: 0105A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)282-7100
TELEFAX: (206)284-6206
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 172
MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGIN: SOURCE:
ORGANISM: Homo sapien
US-08-149-101A-21
Query Match 93.0%; Score 53; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISLR 11
DB 31 RYLDGISLR 41
RESULT 11
PCT-US94-12873-21
Sequence 21 Application PC/TUS9412873
Patent No. 6171824
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Cell Therapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12873
FILING DATE: 8-No. 6171824-1993
SEQUENCE CHARACTERISTICS:
LENGTH: 172
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGIN: SOURCE:
ORGANISM: Homo sapien
US-08-149-101A-21
Query Match 93.0%; Score 53; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISLR 11
DB 31 RYLDGISLR 41
RESULT 12
US-08-149-101A-20
Sequence 20 Application US/08149101A
Patent No. 6171824
GENERAL INFORMATION:

```

APPLICANT: Todaro, George J.
 APPLICANT: Leung, David W.
 APPLICANT: Kose, Timothy M.
 INVENTOR: HIRSH, BRAD CYTOKINES
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 STREET: 200 Elliott Avenue West, Suite 400
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" disk, 1.44MB, double side, high density
 OPERATING SYSTEM: MS-DOS Version 6
 SOFTWARE: WORD for WINDOWS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/097,869
 CLASSIFICATION: 510
 PRIORITY INFORMATION: 6,718,241-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/097,869
 FILING DATE: 27-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Oster, Jeffrey B. and Paciszewski, Stephen
 REGISTRATION NUMBER: 32,585 and 36,131, respectively
 TELEPHONE: (206)282-7100
 TELEFAX: (206)282-7100
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 ANTI-SENSE: no
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: homo sapien
 US-08-149-101A-20

Query Match 93.0%; Score 53; DB 4; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RYLDGISTSLR 11
 Db 31 RYLDGISTSLR 41
 RESULT 13
 PCT-US94-12873-20
 Sequence 20, Application PC/TUS9412873
 GENERAL INFORMATION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TITLE OF INVENTION: HYBRID CYTOKINES
 NUMBER OF SEQUENCES: 26
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" disk, 1.44MB, double side, high density
 OPERATING SYSTEM: MS-DOS Version 6
 SOFTWARE: WORD for WINDOWS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/12873
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:

LENGTH: 174
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US94-12873-20

Query Match 93.0%; Score 53; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RYLDGISTSLR 11
 Db 31 RYLDGISTSLR 41

RESULT 14
 US-08-209-182C-4
 Sequence 4, Application US/08209182C
 GENERAL INFORMATION:
 APPLICANT: Skelly, Susan M.
 APPLICANT: Tackney, Charles T.
 APPLICANT: Snowwaert, John N.
 TITLE OF INVENTION: Foxlikes, Dana M.
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 STREET: 180 Varlock Street
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10014
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/209,182C
 FILING DATE: 10-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/724,698
 FILING DATE: 02-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Felt, Irving N.
 REGISTRATION NUMBER: 28,601
 TELEPHONE/DOCKET NUMBER: SKE-1-PD
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 212-645-2054
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-209-182C-4
 Query Match 93.0%; Score 53; DB 1; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RYLDGISTSLR 11
 Db 27 RYLDGISTSLR 37
 RESULT 15
 PCT-US92-05612-4
 Sequence 4, Application PC/TUS9205612
 GENERAL INFORMATION:

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CC deficiencies eg. myeloma, chronic articular rheumatism and endotoxin
 CC shock. Antagonist comprises Bsp2 peptide (pref. AAs 20-40) with
 CC substitutions of two or more C- and/or N-terminal AAs.
 XX
 XX Sequence 29 AA:

Query Match 100.0%; Score 75; DB 11; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2,7e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 STRVLIQIQRKAKNL 16
 ||||||||||||
 Db 13 STRVLIQIQRKAKNL 28

RESULT 2
 AA002910
 AA002910 standard; Protein: 148 AA.

AC AA002910;
 XX
 XX 12-SEP-2001 (first entry)
 DE Angiotensin converting enzyme (ACEV) splice variant protein #10.

XX Angiotensin converting enzyme splice variant; ACEV; Interleukin 6;
 XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 XX platelet-derived endothelial cell growth factor; cardiovascular disease;
 XX cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
 XX vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 XX myocardial infarction; coronary arterial thrombosis; renal disease;
 XX diabetic nephropathy; muscular disease; rheumatoid arthritis;
 XX insulin resistance; insulin-dependent diabetes mellitus; thrombosis;
 XX noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
 XX vascular disorder; asbestosis.
 XX
 XX Homo sapiens.

OS Homo sapiens.
 XX
 XX MO200136632-42.
 XX
 XX 25-MAY-2001.
 XX
 XX 17-NOV-2000: 2000MO-1100766.

XX 17-NOV-1999: 99IL-0132978.
 XX 10-DEC-1999: 99IL-0134355.
 XX
 XX (COMP-) COMPUGEN LTD.

XX
 XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX WPI: 2001-336004/35.
 XX N-PSDB; AAS06010.
 XX
 XX

XX Novel alternative splicing variants e.g. variant of angiotensin
 XX converting enzyme (ACEV), useful in identifying candidate compounds
 XX capable of binding to the variant and to detect anti-variant antibodies
 XX
 XX
 XX Claim 4: Flg 10: 51pp: English.

XX The sequence represents an angiotensin converting enzyme splice variant
 XX (ACEV) polypeptide. The polypeptides of the invention include variants of
 XX granulocyte colony stimulating factor receptor, glucagon, hypertrophy,
 XX platelet-derived endothelial cell growth factor, cardiovascular disease,
 XX cellular tumour antigen p53, cyclin-dependent kinase inhibitor 1C,
 XX vasoactive intestinal polypeptide receptor 2, arteriosclerosis, cancer,
 XX myocardial infarction, coronary arterial thrombosis, renal disease,
 XX diabetic nephropathy, muscular disease, rheumatoid arthritis,
 XX insulin resistance, insulin-dependent diabetes mellitus, thrombosis,
 XX noncardiotoxic pulmonary granulomatous disease, endothelial abnormality;
 XX vascular disorder, asbestosis. The sequences of
 XX the invention can be used in the treatment and diagnosis of various
 XX disorders including cardiovascular diseases such as arteriosclerosis,
 XX myocardial infarction and coronary arterial thrombosis, renal diseases

CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC cancer, arteriosclerosis, noncardiotoxic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.
 XX
 XX Sequence 148 AA:

Query Match 100.0%; Score 75; DB 22; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 STRVLIQIQRKAKNL 16
 ||||||||||||
 Db 82 STRVLIQIQRKAKNL 97

RESULT 3
 AAR77393
 ID -AAR77393 standard; Protein: 151 AA.

AC AAR77393;
 XX
 XX 17-APR-1996 (first entry)
 DE Human mutant IL-6a/C3 (amino acids 5-19, 44-50 and 73-83 deleted).

XX Human Interleukin-6; IL-6a/C3 mutant; increased stability;
 XX recombinant; production; deletion mutant;
 XX amino acids 5-19, 44-50 and 73-83.
 XX
 XX Homo sapiens.

XX
 XX JPO7224097-A.
 XX
 XX PD 22-AUG-1995.
 XX
 XX 08-FEB-1994: 94JP-0014461.
 XX
 XX 08-FEB-1994: 94JP-0014461.

XX (ASAG) ASahi GLASS CO LTD.
 XX
 XX WPI: 1995-325556/42.
 XX N-PSDB; AAO94348.
 XX
 XX Interleukin-6 mutant, related DNN and expression vectors - has
 XX higher stability than natural Interleukin-6
 XX
 XX
 XX Claim 1: Pages 15-16; 18pp: Japanese.

XX AAO94348 encodes AAR77393 the human IL-6 deletion mutant IL-6a/C3
 XX which lacks the amino acids Gly5-Leu19, Cys44-Cys50 and Cys73-Cys83
 XX of the wild type protein. The cDNA can be used for the recombinant
 XX CC prodn. of IL-6a/C3 which has increased stability compared to wild
 XX type IL-6.
 XX
 XX Sequence 151 AA:

Query Match 100.0%; Score 75; DB 16; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 STRVLIQIQRKAKNL 16
 ||||||||||||
 Db 85 STRVLIQIQRKAKNL 100

RESULT 4
 AAR77392
 ID -AAR77392 standard; Protein: 158 AA.

XX AAR7392: 17-APR-1996 (first entry)
 XX Human mutant IL-6a/C2 (amino acids 5-19 and 73-83 deleted).
 XX Human Interleukin-6; IL-6a/C2 mutant; increased stability;
 XX recombinant; production; deletion mutant;
 XX amino acids 5-19 and 73-83.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX mat_peptide 1..474
 XX /tag= a
 XX JF07224097-A.
 XX 22-AUG-1995.
 XX 08-FEB-1994: 94JP-0014461.
 XX 08-FEB-1994: 94JP-0014461.
 XX 08-FEB-1994: 94JP-0014461.
 XX (ASNG) ASANI GLASS CO LTD.
 XX (ASNG) ASANI GLASS CO LTD.
 XX WPI: 1995-325556/42.
 XX N-PSDM; AAO94347.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 XX higher stability than natural Interleukin-6
 XX Claim 1; Pages 14-15; 18pp; Japanese.
 XX AAO94347 encodes AAR7392, the human IL-6 deletion mutant IL-6a/C2
 XX which lacks the amino acids Gly5-Ileu19 and Cys44-Cys50 of the
 XX wild type protein. The cDNA can be used for the recombinant prodn.
 XX of IL-6a/C2 which has increased stability compared to wild type
 XX IL-6.
 XX Sequence 158 AA:
 SQ
 Query Match 100.08; Score 75; DB 16; Length 158;
 Best Local Similarity 100.08; Pred. No. 0.00014;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKVLIQFTQKKAKN 16
 DB 92 STKVLIQFTQKKAKN 107
 RESULT 5
 AAR7391
 ID AAR7391 standard: Protein; 162 AA.
 AC AAR7391:
 XX 17-APR-1996 (first entry)
 XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).
 XX Human Interleukin-6; IL-6a/C1 mutant; increased stability;
 XX recombinant; production; deletion mutant;
 XX amino acids 5-19 and 44-50.
 XX Homo sapiens.
 XX JF07224097-A.
 XX 22-AUG-1995.
 XX

PF 08-FEB-1994: 94JP-0014461.
 XX 08-FEB-1994: 94JP-0014461.
 XX (ASNG) ASANI GLASS CO LTD.
 XX WPI: 1995-325556/42.
 XX N-PSDM; AAO94346.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 XX higher stability than natural Interleukin-6
 XX Claim 1; Page 14; 18pp; Japanese.
 XX AAO94346 encodes AAR7391, the human IL-6 deletion mutant IL-6a/C1,
 XX which lacks the amino acids Gly5-Ileu19 and Cys44-Cys50 of the
 XX wild type protein. The cDNA can be used for the recombinant prodn.
 XX of IL-6a/C1, which has increased stability compared to wild type
 XX IL-6.
 XX Sequence 162 AA:
 SQ
 Query Match 100.08; Score 75; DB 16; Length 162;
 Best Local Similarity 100.08; Pred. No. 0.00014;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKVLIQFTQKKAKN 16
 DB 96 STKVLIQFTQKKAKN 111
 RESULT 6
 AAM00131
 ID AAM00131 standard: Protein; 162 AA.
 AC AAM00131:
 XX 09-APR-1997 (first entry)
 XX Human Interleukin-6 fragment.
 XX Secretary; signal peptide; P-factor; multicloning vector; PCR;
 XX animal protein; expression; production; recombinant; primer;
 XX cDNA; Schizosaccharomyces pombe; human; human IL-6;
 XX poly(A) tail; chain resection; Schizosaccharomyces pombe;
 XX PO fragment.
 XX Homo sapiens.
 XX MO9623890-A1.
 XX 08-AUG-1996.
 XX 01-FEB-1996: 96MO-JP00198.
 XX 03-FEB-1995: 95JP-0017167.
 XX (ASNG) ASANI GLASS CO LTD.
 XX Hama Y, Kumagai H, Nikaido K, Tohda H, Tsukamoto H;
 XX WPI: 1996-371438/37.
 XX Schizosaccharomyces pombe secretary signal peptide (P-factor) gene
 XX - for production of vectors for expression of animal proteins in a
 XX fission yeast, pref. S. pombe, host
 XX Example 4; Pages 28-29; 50pp; Japanese.
 XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
 XX cDNA, a Schizosaccharomyces pombe secretary signal peptide
 XX fragment, or P-factor fragment (PO fragment) DNA and preferably an

CC animal cell viral promoter sequence and a neomycin resistance gene,
CC can be used for the efficient production of a hIL-6 fragment, i.e.
CC the present sequence, in a fission yeast host, preferably *S. pombe*,
CC culture.

XX Sequence 163 AA:

Query Match 100.0%: Score 75; DB 17; Length 162;

Best Local Similarity 100.0%: Pred. No. 0.00014; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 STKVLQIQLQKAKNL 16

DB 96 STKVLQIQLQKAKNL 111

RESULT 7

AA00132 standard; Protein: 163 AA.

XX AA00132;

XX 09-APR-1997 (first entry)

XX Human Interleukin-6 fragment.

XX Secretory: signal peptide; P-factor; multicloning vector; PCR;

XX animal protein; expression; production; recombinant; primer;

XX fission yeast; human; serum albumin; Interleukin-6;

XX polymerase chain reaction; Schizosaccharomyces pombe;

XX PI fragment.

XX Homo sapiens.

XX MO5623890-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 95MD-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASAMI GLASS CO LTD.

XX Hama Y, Kumagai H, Nakado K, Tohda H, Tsukamoto H;

XX WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene

XX - for production of vectors for expression of animal proteins in a

XX fission yeast, pref. *S. pombe*, host

XX Example 7: Pages 30-31; 50pp; Japanese.

XX A multicloning vector, comprising the human Interleukin-6 (hIL-6)

XX fragment, Schizosaccharomyces pombe secretory signal peptide, an

XX animal cell viral promoter sequence and a neomycin resistance gene,

XX can be used for the efficient production of a hIL-6 fragment, i.e.

XX the present sequence, in a fission yeast host, preferably *S. pombe*,
XX culture.

XX Sequence 163 AA:

Query Match 100.0%: Score 75; DB 17; Length 163;

Best Local Similarity 100.0%: Pred. No. 0.00014; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 STKVLQIQLQKAKNL 16

DB 97 STKVLQIQLQKAKNL 112

RESULT 8

AA077390 standard; Protein: 166 AA.

XX AA077390;

XX 17-APR-1996 (first entry)

XX Human IL-6 mutant IL-6C3 (amino acids 44-50 and 73-83 deleted).

XX Human Interleukin-6; IL-6C3 mutant; increased stability;

XX recombinant; production; deletion mutant;

XX amino acids 44-50 and 73-83.

XX Homo sapiens.

XX Key

XX mal-peptide

XX 1,498

XX /tag- a

XX JP07224097-A.

XX 22-AUG-1995.

XX 08-FEB-1994; 94JP-0014461.

XX 08-FEB-1994; 94JP-0014461.

XX (ASAG) ASAMI GLASS CO LTD.

XX WPI: 1995-325556/42.

XX N-PSDB: AA094345.

XX Interleukin-6 mutant, related DNA and expression vectors - has

XX higher stability than natural Interleukin-6

XX Claim 1: Page 13; 18pp; Japanese.

XX AA094345 encodes AA077390 the human IL-6 deletion mutant IL-6C3,

XX which lacks the amino acid residues 44-50 and 73-83, and is a recombinant prodn.

XX of IL-6C3, which has increased stability compared to wild type

XX IL-6.

XX CC

XX SO

XX Sequence 166 AA:

Query Match 100.0%: Score 75; DB 15; Length 166;

Best Local Similarity 100.0%: Pred. No. 0.00015; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 STKVLQIQLQKAKNL 16

DB 100 STKVLQIQLQKAKNL 115

RESULT 9

AA077649 standard; Protein: 167 AA.

XX AA077649;

XX 27-JUN-1996 (first entry)

XX Human Interleukin-6 splice variant.

XX Human; interleukin-6; splice variant; IL-6SV; treatment;

XX immunotherapy; side effect; corneal damage; keratitis; ulcer;

XX chemotherapeutic; multiple myeloma;

XX antitumor; Castleman's disease; rheumatoid arthritis;

XX cardiac myxoma; cervical cancer; rheumatoid arthritis;

[illegible]

Human Interleukin-6; IL-6C2 mutant; increased stability;
recombinant; production; deletion mutant; amino acids 73-83.

XX	Homo sapiens.
OS	
XX	
FX	
FT	
Key	Location/Qualifiers
mat_peptide	1..519

FI	/ *La9	a
XX		
PN	JP07224097-A.	
XX		

PD	22-AUG-1995.
XX	
PF	08-FEB-1994.
XX	
PR	08-FEB-1994.
	94UP-0014461.

XX (ASAG) ASAHI GLASS CO LTD.
PA .
XX
XX
DR WPI: 1995-32556/42.

XX N-PSDB: AAQ94344.
XX
XX Interleukin-6 mutant, related DNA and expression vectors - has
PT higher stability than natural Interleukin-6
XX

PS Clalm 1, Page 12; 18pp; Japanese.
XX
CC AAQ94344 encodes AAR77389 the human IL-6 deletion mutant IL-6C2,
CC which lacks the amino acids Cys73-Cys83 of the wild type protein.

CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
CC has increased stability compared to wild type IL-6.
CC
XX
SQ Sequence 173 AA:

Query Match 100.0%; Score 75; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLTOPLOKRAKML 16
 |||||||
 DB 107 SKVLTLQIGKAKML 122

RESULT 12

ID AAR75342 standard: Protein: 174 AA.

AC AAR75342:

DE 13-DEC-1995 (first entry)

XX Hybrid human cytokine IIII.

XX Hybrid cytokine: tumour proliferation; cancer therapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 173 /note= "Site of stop codon"

XX MO9513393-A.

XX 18-MAY-1995.

XX 07-NOV-1994: 94WO-US12873.

XX 08-NOV-1993: 93US-0149101.

XX (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

XX Leung DM, Rose TM, Todaro GJ:

XX WPI: 1995-194111/25.

XX N-PSDB: AA087161.

XX New hybrid cytokines with alpha helical sequences from different

XX sources - also DNA encoding them, vectors and transformed cells,

XX useful e.g. for treating cancer, remodelling bone etc.

XX Claim 11: Page 31: 52pp: English.

XX The cytokine encoding genes for leukemia inhibitory factor (L),

XX granulocyte-colony stimulating factor (G), interleukin-6 (I),

XX interleukin-11 (E), ciliary neurotrophic factor (C) and

XX oncostatin M (O) have been cloned and reported in the literature.

XX CC provides a group of therapeutic hybrid cytokines having a size ranging

XX from about 10 to about 30 kDa. Each hybrid cytokine comprises three or

XX four alpha-helical sequences and linking sequences, ranging from about

XX 5-40 AAs in length. In the nomenclature of the hybrid cytokines,

XX CC letters designate alpha-helical sequences, lower case

XX letters designate linking sequences. The first three alpha-helical

XX sequences of IIII and IIII-alpha were derived from IL-6 and the

XX fourth alpha-sequence was derived from LIF. IIII-alpha has two

XX additional AAs inserted in a linking sequence between alpha-helices

XX III and IV, as compared with IIII.

XX Sequence 174 AA:

Query Match 100.0%; Score 75; DB 16; Length 174;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLTOPLOKRAKML 16
 |||||||
 DB 119 SKVLTLQIGKAKML 134

RESULT 13

ID AAR75341 standard: Protein: 176 AA.

AC AAR75341:

DE 13-DEC-1995 (first entry)

XX Hybrid human cytokine IIII-alpha.

XX Hybrid cytokine: tumour proliferation; cancer therapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 175 /note= "Site of stop codon"

XX MO9513393-A.

XX 18-MAY-1995.

XX 07-NOV-1994: 94WO-US12873.

XX 08-NOV-1993: 93US-0149101.

XX (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

XX Leung DM, Rose TM, Todaro GJ:

XX WPI: 1995-194111/25.

XX N-PSDB: AA087160.

XX New hybrid cytokines with alpha helical sequences from different

XX sources - also DNA encoding them, vectors and transformed cells,

XX useful e.g. for treating cancer, remodelling bone etc.

XX Claim 11: Page 30: 52pp: English.

XX The cytokine encoding genes for leukemia inhibitory factor (L),

XX granulocyte-colony stimulating factor (G), interleukin-6 (I),

XX interleukin-11 (E), ciliary neurotrophic factor (C) and

XX oncostatin M (O) have been cloned and reported in the literature.

XX CC provides a group of therapeutic hybrid cytokines having a size ranging

XX from about 10 to about 30 kDa. Each hybrid cytokine comprises three or

XX four alpha-helical sequences and linking sequences, ranging from about

XX 5-40 AAs in length. In the nomenclature of the hybrid cytokines,

XX CC letters designate alpha-helical sequences, lower case

XX letters designate linking sequences. The first three alpha-helical

XX sequences of IIII and IIII-alpha were derived from IL-6 and the

XX fourth alpha-sequence was derived from LIF. IIII-alpha has two

XX additional AAs inserted in a linking sequence between alpha-helices

XX III and IV, as compared with IIII.

XX Sequence 176 AA:

Query Match 100.0%; Score 75; DB 16; Length 176;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLTOPLOKRAKML 16
 |||||||
 DB 119 SKVLTLQIGKAKML 134

RESULT 14

```

XX 1 Leung DW, Rose TM, Todaro GJ:
DR WPI: 1995-194111/25.
XX N-PDB: AAC87153.
XX
XX Now hybrid cytokines with alpha helical sequences from different
XX sources - also DNA encoding them, vectors and transformed cells,
XX useful e.g. for treating cancer, remodelling bone etc.
XX
XX Disclosure: Page 23-24, 52pp: English.
XX
XX The cytokine encoding genes for leukemia inhibitory factor (LIF),
XX interleukin-6 (IL-6), oncostatin factor (OSF), granulocyte colony-stimulating factor (G-CSF),
XX interleukin-11 (IL-11), colony neutrophilic factor (CNF) and
XX oncostatin-M (OSM) have been cloned and reported in the literature.
XX IL-6, G-CSF, LIF, IL-11, CNF and OSM each comprise four alpha-
XX helical sequences. In each cytokine, the four alpha-helical
XX sequences are linked by non-alpha-helical 'linking' sequences of
XX about 5-100 Aas, and in some cases the alpha-helices are maintained
XX in the proper conformation and geometry with respect to each other
XX through disulfide bridges. The invention provides a group of
XX hybrid cytokines, each having at least one alpha-helical sequence
XX to about 30 kDa. Each hybrid cytokine comprises three or four
XX alpha-helical sequences and linking sequences, ranging from about
XX 5-40 Aas in length, selected from the linking sequences of the
XX above cytokines or other linking sequences.
XX
XX Sequence 179 Aa:
SQ
XX
XX Query Match 100.0%; Score 75; DB 16; Length 179;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
XX
XX QY 1 SFKVLQIFLOKKRANL 16
XX |||||||
XX DB 113 SFKVLQIFLOKKRANL 128

```


A:Note: sequence extracted from NCBI backbone
A:Note: this 28-30K form contained both N-linked and O-linked carbohydrate: a 25K form
A:Accession: C48419
A:Molecule type: protein
A:Source: human (Homo sapiens)
A:Note: sequence extracted from NCBI backbone (NCBI:63787)
A:Note: this 23-25K form contained O-linked but not N-linked carbohydrate
R:Orth, T.; Oheda, M.; Hasegawa, M.; Kubonatu, H.; Esaki, K.; Ochi, N.
J. Biochem. 115, 345-350, 1994
A:Title: Polypeptide and carbohydrate structure of recombinant human Interleukin-6 protein
A:Accession number: J05050; accession: J05050
A:Reference number: J05050; accession: J05050
R:Clodogne, C.L.; Boone, T.C.; Candell, C.; Mendiaz, E.A.; Lu, H.S.
Arch. Biochem. Biophys. 272, 14-151, 1989
A:Title: Disulfide structures of human interleukin-6 are similar to those of human granin
A:Accession number: 504981; M01D: 89286115
A:Contents: annotation; disulfide bonds in recombinant protein
R:ROCK, F.L.; Li, X.; Gong, J.; Ida, R.; Klein, M.
J. Biol. Chem. 268, 1515-1520, 1993
A:Title: Roles of disulfide bonds in recombinant human interleukin-6 conformation.
A:Reference number: A54253; M01D: 91227004
A:Contents: annotation; lability and functional significance of each disulfide bond
C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor
Lbulin secretion). It therefore appears to function as an autoregulator of cell growth
C:Comment: This protein plays a regulatory role in various host defense mechanisms and
C:Accession: J116
A:Cross-references: GDB:120748; OMIM:147620
A:Map position: 7p21-7p21
A:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth factor
E:1-17/Domain: signal sequence; status predicted <SIG>
E:18-212/Product: interleukin-6, long form [status experimental <MUTD>
E:22-78,101-111/Disulfide bonds: #status experimental <MUTD>
E:173/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
E:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
E:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 212;
Local Similarity 11.0%; E-Value 0.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 STKYLTFLOKRAKNL 16
|||||

Db 146 STKYLTFLOKRAKNL 161

2
T09216
Interleukin-6 precursor - horse
C:Species: Equus caballus (domestic horse)
C>Date: 11-Jun-1999 #sequence: revision 11-Jun-1999 #text_change 23-Jul-1999
C:Accession: T09216
R:Smideraki, C.E.; Kotchov, D.W.
A:Reference number: J16613; accession: J16613
A:Accession: T09216
A:Status: Preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: RNA
A:Residues: 1-208 <SWI>
C:Genetics:
C:Gene:
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor

Query Match 66.7%; Score 50; DB 2; Length 208;
Best Local Similarity 66.7%; Prnd. 0.31;

Matches 10: Conservative 2: Mismatches 3: Indels 0: Gaps 0:

Query 1 STVYIOPFOKKAKN 15
 |||||:|:|:|:|
 Db 143 STVYIOPFOKKAKN 157

RESULT 3
 146084
 Interleukin 6 - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 16-Aug-1997 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
 C:Accession: F14621
 R:Bradley, W.G.; Gibbs, C.; Kraus, I.; Good, R.A.; Day, N.K.
 Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
 A:Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6
 A:Reference number: 146084; MID:94052249
 A:Accession: 146084
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <R1C>
 A:Cross-references: GB:146094; NID:q438519; PIDN:AA16620.1; PID:q438520
 C:Superfamily: Interleukin-6

Query Match 62.7% Score 47; DB 2; Length 207;
 Best Local Similarity 60.0% Pred. No. 1;
 Matches 10: Conservative 3: Mismatches 3: Indels 0: Gaps 0:

Query 1 STVYIOPFOKKAKN 15
 |||||:|:|:|:|
 Db 142 STVYIOPFOKKAKN 156

RESULT 4
 146621
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146621
 R:Richards, C.; Saklatvala, J.
 Cytochrome 3, 265-276, 1991
 A:Reference number: 146621; MID:91338547
 A:Accession: 146621
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <R1C>
 A:Cross-references: GB:M6722; NID:q164624; PIDN:AMC3733.1; PID:q164625
 C:Genetics:
 C:Superfamily: Interleukin-6

Query Match 62.7% Score 47; DB 2; Length 212;
 Best Local Similarity 66.7% Pred. No. 1;
 Matches 10: Conservative 2: Mismatches 3: Indels 0: Gaps 0:

Query 1 STVYIOPFOKKAKN 15
 |||||:|:|:|:|
 Db 146 STVYIOPFOKKAKN 160

RESULT 5
 146590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146590
 R:Mahalingam, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conce
 A:Reference number: 146590; MID:92360284

A:Accession: 146590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <R1C>
 A:Cross-references: GB:M60258; NID:q164514; PIDN:AMC27127.1; PID:q164515
 C:Genetics:
 C:Superfamily: Interleukin-6

Query Match 62.7% Score 47; DB 2; Length 212;
 Best Local Similarity 66.7% Pred. No. 1;
 Matches 10: Conservative 2: Mismatches 3: Indels 0: Gaps 0:

Query 1 STVYIOPFOKKAKN 15
 |||||:|:|:|:|
 Db 146 STVYIOPFOKKAKN 160

RESULT 6
 F81448
 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) [Cyt298c [imported]] - C
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C:Accession: F81448
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chl
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
 Nature 403, 665-668, 2000
 A:Reference: the genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A:Accession: F81448
 A:Residues: 1-274 <P4K>
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-274 <P4K>
 A:Cross-references: GB:AL13074; GB:AL111168; NID:56967505; PIDN:CAM72765.1; PID:q596
 A:Experimental source: serotype O2, strain NCTC 11168
 A:Gene: pamb; C10298c
 C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
 C:Keywords: coenzyme A biosynthesis; transferase

Query Match 61.3% Score 46; DB 2; Length 274;
 Best Local Similarity 69.2% Pred. No. 1.9;
 Matches 5: Conservative 2: Mismatches 2: Indels 0: Gaps 0:

Query 3 KVIYIOPFOKKAKN 15
 |||||:|:|:|:|
 Db 3 KSMISFLEKKAKN 15

RESULT 7
 B71405
 Probable kinasin - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: B71405
 R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgamen
 erfahrt, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechmann, S.;
 C.; Chalvatzis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
 A:Accession: B71405
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-959 <REV>
 A:Cross-references: GB:297336; NID:q2244788; PIDN:CAM10212.1; PID:q2244790
 C:Genetics:

R:Decker G.; Warren, P.V.; Gaasterland, W.G.; Lenox, A.L.; Graham, D.E.
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-May-2000
C:Accession: G70355

Genome version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:13 ; Search time 48.45 seconds
(without alignments)
12.108 Million cell updates/sec

Title: US-09-202-104a-2

Sequence: 1 STKVLIQFLQKKAKNL 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36654827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	212	1	IL6_HUMAN
2	75	100.0	212	1	IL6_MACAC
3	75	100.0	212	1	IL6_MACMU
4	75	92.0	208	1	IL6_CERO
5	75	92.0	208	1	IL6_HORSE
6	50	66.7	208	1	IL6_MOUSE
7	47	62.7	208	1	IL6_FELCA
8	47	62.7	209	1	IL6_PHOVI
9	47	62.7	212	1	IL6_PIG
10	42	56.0	161	1	IL255_BUCAL
11	40	53.3	205	1	IL6_MOUSE
12	39	53.3	205	1	IL6_MOUSE
13	39	53.3	205	1	IL6_MOUSE
14	39	52.0	487	1	ATF2_CHICK
15	39	52.0	487	1	ATF2_HUMAN
16	39	52.0	487	1	ATF2_MOUSE
17	39	52.0	487	1	ATF2_RAT
18	39	52.0	704	1	DBF1_YEAST
19	39	52.0	704	1	DBF1_YEAST
20	39	52.0	704	1	DBF1_YEAST
21	39	52.0	704	1	DBF1_YEAST
22	38	50.7	130	1	RS22_YEAST
23	38	50.7	130	1	RS22_YEAST
24	38	50.7	657	1	YWR4_CHIMP
25	38	50.7	3144	1	DBP1_HUMAN
26	38	50.7	3144	1	DBP1_HUMAN
27	37.5	50.0	1081	1	DBP1_HUMAN
28	37.5	50.0	1081	1	DBP1_HUMAN
29	37	49.3	187	1	YWR4_HUMAN
30	37	49.3	220	1	YWR4_HUMAN
31	37	49.3	346	1	MGRL_HUMAN
32	37	49.3	436	1	ACRO_HUMAN
33	37	49.3	458	1	ACRO_HUMAN

34	37	49.3	1049	1	POL_HV261
35	37	49.3	1073	1	POL_HV261
36	37	49.3	1142	1	POL_HV261
37	36.5	48.7	155	1	FBAT_ZYMO
38	36	48.0	227	1	Y03_MERTU
39	36	48.0	246	1	PSA6_SOYBN
40	36	48.0	246	1	PSA6_SOYBN
41	36	48.0	246	1	PSA6_SOYBN
42	36	48.0	374	1	HSP67_HUMAN
43	36	48.0	856	1	CLP4_HUMAN
44	36	48.0	856	1	CLP4_HUMAN
45	36	48.0	1477	1	FOR1_YEAST

ALIGNMENTS

RESULT	1	STANDARD	PRT	212 AA
AD	IL6_HUMAN			
AD	P05231			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DE	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)			
DE	(INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)			
GN	IL6 OR IFNB2			
OS	Human sapiens (human)			
OC	Mammalia: Eutheria: Chordata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo			
NCBI_TaxID	9606;			
OX	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	SEQUENCE-87065033; PubMed-3491322;			
RA	Hirano T., Yasukawa K., Hatada H., Taga T., Matsuda T.,			
RA	Kashiyama S., Nakai H., Nakai H., Koyama K., Ikenatsu A., Ikenatsu S.,			
RA	Yasukawa K., Nakai H., Nakai H., Koyama K., Ikenatsu A., Ikenatsu S.,			
RA	"Structure and expression of human B cell stimulatory factor-2			
RT	(BSF-2/IL-6) gene.";			
RL	EMBO J. 6:2939-2945(1987).			
RL	Nature 324:73-76(1986).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE-87067433; PubMed-3538015;			
RA	Wang L.T., Helgort D.C., Sehgal P.B.,			
RA	"Structure and expression of human B cell stimulatory factor-2			
RT	structural studies of the beta 2 interferon involved.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE-87053818; PubMed-3023045;			
RA	Wang L.T., Helgort D.C., Sehgal P.B.,			
RA	"Structure and expression of human B cell stimulatory factor-2			
RT	structural studies of the beta 2 interferon involved.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).			
RL	[5]			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE-87068766; PubMed-3330204;			
RA	Ardien J.A., U.P.O., de Groot E.R., Evers R.F., Pannekoek H.,			
RA	"Molecular cloning and expression of hybridoma growth factor in			
RT	Escherichia coli.";			
RT	J. Immunol. 139:4116-4121(1987).			
RL	[6]			

RP SEQUENCE FROM N.A.
 RX MEDLINE-89391328: PubMed-2789313.
 RA "Production of a recombinant region of human BSP-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells."
 RL Blochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-91246342: PubMed-3758081.
 RA Heesman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Flats M.
 RA "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts."
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [18]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-89193117: PubMed-3266663.
 RA Wong G., Witke-Glanoff J., Hewick R., Clark S., Ogawa M.,
 RA "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor."
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [19]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-93178270: PubMed-1291290.
 RA Chen O. Y. J.
 RA "Stable and efficient expression of human Interleukin-6 cDNA in
 RT mammalian cells after gene transfer."
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RN SEQUENCE OF 30-63
 RX MEDLINE-95154445: PubMed-3279116.
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.
 RA "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6."
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RN SEQUENCE OF 50-212 OF RECOMBINANT FROM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE-95154944: PubMed-7851440.
 RA Breton J., la Fluta A., Bertolero F., Orsini G., Valsassina B.,
 RA Zillicotto R., de Filippis V., Polverio de Laureto P., Fontana A.;
 RA "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human Interleukin-6 containing a single
 RT disulfide bond."
 RL J. Biochem. 227:573-581(1995).
 RN [12]
 RN DISULFIDE BONDS.
 RX MEDLINE-89286115: PubMed-2472117.
 RA Clogston C. L., Boone T. C., Crandall B. C., Mendiaz E. A., Lu H. S.;
 RA "Disulfide structures of human Interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor."
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RN MEDICINE.
 RX MEDLINE-91243808: PubMed-2037043.
 RA Luetticken C., Kruecken A., Moellner A., Rose-John S.;
 RA "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6."
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RN STRUCTURE BY NMR.
 RX MEDLINE-96134845: PubMed-8555185.
 RA Nishimura G., Matsubae A., Gonda H., Shimada I., Arata Y.;
 RA "Folding topologies of human Interleukin-6 and its mutants as studied
 RT by NMR spectroscopy."
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RN STRUCTURE BY NMR.
 RX MEDLINE-97303053: PubMed-9159484.

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA "Solution structure of recombinant human Interleukin-6."
 RT J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97224126: PubMed-9118960.
 RA Somers W., Stahl M., Seeha J. S.;
 RA "The crystal structure of human Interleukin 6: implications for a novel
 RT type of cytokine dimerization and signaling."
 RL BMO J. 16:989-997(1997).
 CC -1 FUNCTION: 116 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO T2-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC REPRODUCTION. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC -1- INDUCES NERVE CELLS DIFFERENTIATION, IN
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 CC -----
 CC EMBL: X04430: CAA28026.1; -
 CC EMBL: M14584: AAB2728.1; -
 CC EMBL: X04602: CAA28268.1; -
 CC EMBL: Y00081: CAA68278.1; -
 CC EMBL: M14403: AAB2728.1; -
 CC EMBL: X04402: CAA27950.1; -
 CC EMBL: X04403: CAA27951.1; -
 CC EMBL: M54894: AAC41704.1; -
 CC EMBL: S56892: AAD33886.1; -
 CC EMBL: A09363: CAA00839.1; -
 CC PIR: A32648: IY0052.
 CC PIR: A32921: AY0052.
 CC PDB: 1IE6: 04-FEB-98.
 CC PDB: 21I6: 04-FEB-98.
 CC PDB: 1ALU: 03-JUN-98.
 DR MIM: 147620: -
 DR InterPro: IPR003573: IL6_MGF_GCSF.
 DR InterPro: IPR003574: Interleukin-6.
 DR Pfam: PF00489: IL6; 1.
 DR PRINTS: PR00433: INTERLEUKIN6.
 DR PRODOM: PD004356: Interleukin-6; 1.
 DR SMART: SM00126: IL6; 1.
 DR PROSITE: PS00254: INTERLEUKIN_6; 1.
 DR CYTOKINE: Glycoprotein; Growth factor; Signal; 3D-structure.
 RT SIGNAL
 FT CHAIN 30
 FT DISULFID 12
 FT DISULFID 103
 FT CARBOHYD 73
 FT MUTAGEN 173
 FT MUTAGEN 185
 FT MUTAGEN 204
 FT MUTAGEN 210
 FT MUTAGEN 212
 SO SEQUENCE 212 AA; 23718 MW; 17EDFEB1B34079 CRC64;
 Query Match 100.0%; Score 75; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3; 8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 STRVLDFLOLRKAKL 16
 146 STRVLDFLOLRKAKL 161


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RESULT 2
ID IL6_MACCA STANDARD; PRT: 212 AA.
AC P79341
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
IL6.
Macaca fascicularis (Cebu eating macaque) (Cynomolgus monkey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
NCBI_TaxID=9541;
OK [1]
RN SEQUENCE FROM N.A.
RA Tarsaul M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC ACTIONS. IT IS AN INDUCER OF INTERLEUKIN-6. IT INDUCES
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOID
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
CC EMBL: AB000534; BA19148.1; -
CC DR HS5P; P05231; 1447; IL6.MGF GCSF
CC DR INTCRPO; IP8003574; Interleukin_6.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PR00433; IL6GCSFNGF.
CC DR PRODOM: P000436; INTERLEUKIN6.
CC DR SMART: SM00126; IL6; 1.
CC DR PROSITE: PS000524; INTERLEUKIN_6_1.
CC DR CYTOKINE; Glycoprotein growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 N-LINKED (GLCNCNC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNCNC. . .) (POTENTIAL).
CC FT SCDENCE 212 AA: 23654 MW: 41105F06C9C0CDD CRC64;
CC
CC Query Match 100.0%; Score 75; DB 1; Length 212;
CC Best Local Similarity 100.0%; Pred. NO. 3,8e-06;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC DB 146 STYVLIOFLOKXANN 161

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecoidea; Macaca.
CC NCBI_TaxID=9541;
CC DR HS5P; P05231; 1447; IL6.MGF GCSF
CC DR INTCRPO; IP8003574; Interleukin_6.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PR00433; IL6GCSFNGF.
CC DR PRODOM: P000436; INTERLEUKIN6.
CC DR SMART: SM00126; IL6; 1.
CC DR PROSITE: PS000524; INTERLEUKIN_6_1.
CC DR CYTOKINE; Glycoprotein growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 N-LINKED (GLCNCNC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNCNC. . .) (POTENTIAL).
CC FT SCDENCE 212 AA: 23728 MW: 41105F06C9C0CDD CRC64;
CC
CC Query Match 100.0%; Score 75; DB 1; Length 212;
CC Best Local Similarity 100.0%; Pred. NO. 3,8e-06;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC DB 146 STYVLIOFLOKXANN 161

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RESULT 3
ID IL6_MACCA STANDARD; PRT: 212 AA.
AC P79341
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
IL6.
Macaca mulatta (Rhesus macaque).
OS

```

```

RESULT 4
ID IL6_CERTO STANDARD; PRT: 212 AA.
AC P79341
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
IL6.
Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
NCBI_TaxID=9541;
RN SEQUENCE FROM N.A.
RA STRAIN-FUJ;

```

EX MEDLINE-96003435; PubMed-7561102;
 RA Villinger F.J., Bear S.S., Mayne A.E., Chikala N., Ansell A.A.;
 RA Comparative sequence analysis of cytokine genes from human and
 RA mouse fibroblasts.
 RL J Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO Ig-SECRETING CELLS. IT INDUCES MYELOID AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
 CC HEPA TOXICITY BELONGS TO THE IL-6 SUPERFAMILY. (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 CC EMBL: U12234; AAA93030.1; -
 DR HSSP: P05231; 2145; IL6_MGF_GCFP.
 DR InterPro: IPR003573; IL6_MGF_GCFP.
 DR InterPro: IPR003574; Interleukin-6.
 DR Pfam: PF00489; IL6; IL6CSMPF.
 DR PRINTS: PR00433; IL6CSMPF.
 DR PRINTS: PR00435; Interleukin-6.
 DR ProDom: PD004356; Interleukin-6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 KM SIGNAL: 1 29
 FT CHAIN: 30 272
 FT DISULFID: 70 718
 FT DISULFID: 101 113
 FT CARBOHYD: 73 73
 FT CARBOHYD: 172 172
 SEQUENCE 212 AA; 23668 MW; C7303525B44B9F CRC64;
 Query Match Best Local Similarity 92.0%; Score 69; DB 1; Length 212;
 Best Local Similarity 93.8%; Prod. No. 4 e-05; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 STKVLDFLOPKKKNL 16
 Db 146 STKVLDFLOPKKKNL 161
 RESULT 5
 ID IL6_CANPA STANDARD; PRT: 207 AA.
 AC P41323;
 DT 01-FEB-1995 (Ref. 31, Created)
 DT 01-FEB-1995 (Ref. 31, Last sequence update)
 DT 15-JUL-1998 (Ref. 36, Last annotation update)
 DE INTERLEUKIN-6 PROCURSOR (IL-6).
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 MX NCBI_Taxid=9615;
 (1)
 RN SEQUENCE FROM N.A.
 RP Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 RA Kunkel G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
 RA Michael L.H., Ballantyne C.M., Smith C.W., Enman M.L.;
 RA "Regulation of ICM-1 and IL-6 in myocardial ischemia: effect of
 RA reperfusion.";
 RA Ann. N.Y. Acad. Sci. 723:258-270(1994).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO Ig-SECRETING CELLS. IT INDUCES MYELOID AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
 CC HEPA TOXICITY BELONGS TO THE IL-6 SUPERFAMILY.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 CC EMBL: U12234; AAA93030.1; -
 DR HSSP: P05231; 2145; IL6_MGF_GCFP.
 DR InterPro: IPR003573; IL6_MGF_GCFP.
 DR InterPro: IPR003574; Interleukin-6.
 DR Pfam: PF00489; IL6; IL6CSMPF.
 DR PRINTS: PR00433; IL6CSMPF.
 DR PRINTS: PR00434; INTERLEUKIN_6; 1.
 DR ProDom: PD004356; Interleukin-6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 KM SIGNAL: 1 29
 FT CHAIN: 30 272
 FT DISULFID: 67 73
 FT DISULFID: 96 106
 SEQUENCE 207 AA; 22945 MW; 4540154E9C0P50 CRC64;
 Query Match Best Local Similarity 66.7%; Score 50; DB 1; Length 207;
 Best Local Similarity 60.0%; Prod. No. 0.097;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 STKVLDFLOPKKKN 15
 Db 141 STKVLDFLOPKKKN 155
 RESULT 6
 ID IL6_HORSE STANDARD; PRT: 208 AA.
 AC O95181; O19007; O46568;
 DT 01-NOV-1997 (Ref. 35, Created)
 DT 15-JUL-1998 (Ref. 38, Last sequence update)
 DT 15-JUL-1998 (Ref. 38, Last annotation update)
 DE INTERLEUKIN-6 PROCURSOR (IL-6).
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 MX NCBI_Taxid=9796;
 (1)
 RN SEQUENCE FROM N.A.
 RP Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 RA Leutenegger C.M., Under J.B., von Rechenberg B., Akens M., Auer J.;
 RA Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RM (12)
 RN SEQUENCE FROM N.A.
 RP Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 RA "Cloning and expression of equine interleukin-6.";
 RA Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO Ig-SECRETING CELLS. IT INDUCES MYELOID AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
 CC HEPA TOXICITY BELONGS TO THE IL-6 SUPERFAMILY.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL: U64794; AAB87703.1; -
 DR EMBL: AF005227; AAB62346.1; -
 DR EMBL: AF041975; AAC04574.1; -
 DR HSSP: P05231; 21L6.
 DR Interpro: IPR003574; IL6_MGF_GCSF.
 DR Pfam: PF004489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSF.
 DR PRODOM: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE: Glycoprotein; Growth factor; Signal.
 FT CHAIN 28 208
 FT SIGNAL 1 27
 FT DISULFID 69 75
 FT DISULFID 98 108
 FT CARBOHYD 71 71
 FT CARBOHYD 184 184
 FT COMFLICT 8 3
 FT COMFLICT 137 137
 FT COMFLICT 205 205
 FT SEQUENCE 208 AA; 23325 MW; A62MAC234056H66 CMC64;

Query Match 66.7%; Score 50; DB 1; Length 208;
 Best Local Similarity 66.7%; Pred.No. 0.997; 3; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 3;

QY 1 STKVLIQFLOKRAKN 15
 DB 143 STKVLIQFLOKRAKN 157

RESULT 7
 ID IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT INTERLEUKIN-6 PRECURSOR (IL-6).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RX MEDLINE=96153018; PubMed=871820;
 RA Hasenauer A.; Wenzel R.; Goltz R.; Tsujimoto H.;
 RL "Molecular cloning of feline interleukin-6 cDNA."
 J. Vet. Med. Sci. 55:941-944(1993).
 RN SEQUENCE FROM N.A.
 RC TISSUE=lymphocytes; pubmed=871820;
 RA Bradley M.G.; Gibbs C.; Kraus J.; Good R.A.; Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 interleukin-6."
 Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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DR EMBL: I16914; AAA16570.1; -
 DR EMBL: D13227; BAA02507.1; -
 DR HSSP: P05231; 21L6.
 DR Interpro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF004489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSF.
 DR PRODOM: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE: Glycoprotein; Growth factor; Signal.
 FT CHAIN 28 208
 FT SIGNAL 1 27
 FT DISULFID 69 75
 FT DISULFID 98 108
 FT CARBOHYD 71 71
 FT CARBOHYD 184 184
 FT COMFLICT 8 3
 FT COMFLICT 133 133
 FT COMFLICT 173 187
 FT SEQUENCE 208 AA; 23401 MW; 53B4450B25950AC CMC64;

Query Match 62.7%; Score 47; DB 1; Length 208;
 Best Local Similarity 60.0%; Pred.No. 0.33;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKRAKN 15
 DB 142 STKVLIQFLOKRAKN 156

RESULT 8
 ID IL6_PROV1 STANDARD; PRT; 209 AA.
 AC Q28819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
 NCBI_TaxID=9720;
 RX MEDLINE=96153018; PubMed=8575817;
 RA King D.P.; Schrenzel M.D.; McKnight M.L.; Reldarsen T.H.; Hanni K.D.;
 RA Scott J.L.; Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 immunogenetics 43:100-105(1996)."
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

```
CC      HEPATOBLASTS IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC      -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      modified and this statement is not removed, usage by and for commercial
CC      entities requires a license agreement (see http://www.isb.ac.uk/announce/
CC      or send an email to licenses@isb.sib.ch).
CC      DR    EMBL: I46802; AB01430.1; -.
CC      DR    HSBP: P05231; IL6.
CC      DR    InterPro: IPRO03573; IL6_MGF_GCSF.
CC      DR    InterPro: IPRO03574; Interleukin_6.
CC      DR    Pfam: PF00489; IL6; 1.
CC      DR    SMART: SM00126; IL6; 1.
CC      DR    PROSITE: PS00234; INTERLEUKIN_6; 1.
CC      DR    PROSITE: PS00234; Growth factor: Signal.
CC      FT     NON_TER
CC      FT     SIGNAL          <1       26       BY SIMILARITY.
CC      FT     CHAIN           27       209      INTERLEUKIN-6.
CC      FT     DISULFID        69       75       BY SIMILARITY.
CC      FT     DISULFID        96       108      BY SIMILARITY.
CC      SEQUENCE             209 AA; 23483 MW; 75144922E3A3B485 CRC64;
CC
CC      Query Match              63.7%; Score 47; DB 1;
CC      Best local similarity   60.0%; Pred. No. 0.33;
CC      Matches               9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC
Oy      1 STVALDIFLOKANN 15
Oy      |||||:|||||:
Db      143 STKLDMKKMKVNS 157
Cc
Cc      RESULT 9
Cc      ID IL6_PIG STANDARD; PROT. 212 AA.
Cc      AC P26893;
Cc      DT 01-AUG-1992 (rel. 3; Created)
Cc      DT 15-DEC-1998 (rel. 37; Last sequence update)
Cc      DT 15-DEC-1998 (rel. 37; Last annotation update)
Cc      GN INTERLEUKIN-6 PRECURSOR (IL-6).
Cc      GN IL6.
Cc      OS Sus scrofa (Pig).
Cc      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc      OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
Cc      OX NCBI_TaxId=9692;
Cc      RX MEDLINE:P0338547; PubMed:1873476;
Cc      RP SPOTLIGHT FROM N.A.
Cc      RX MEDLINE:P0338547; PubMed:1873476;
Cc      RX Molecular cloning and sequence of porcine interleukin 6 cDNA and
Cc      expression of mRNA in synovial fibroblasts in vitro *;
Cc      Cytokine 3:269-276(1991).
Cc      RA SOURCE FROM N.A.
Cc      RN MEDLINE:92360284; PubMed:1497880;
Cc      RA Methiasian N., Bixby J.A., Roberts M.R.;
Cc      RT Expression of Interleukin-6 in porcine, ovine, and bovine
Cc      RT preimplantation conceptuses *;
Cc      MO1. Reprint. Dev. 32:334-330(1992).
Cc      RT FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
Cc      FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
Cc      OF T CELLS INTO TH1 AND TH2 SUBSETS AND IN THE REGULATION OF
Cc      PLASMACYTIC GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
Cc      HEPATOCYTES IT INDICES ACUTE PHASE REACTANTS.
Cc      -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
Cc
Cc      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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```

[illegible]

Query Match
Best Local Similarity 56.0%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 VILOPLOCKANN 15
DB 142 ILVNFORKANN 153

RESULT 11

IL6-ORC9C STANDARD; PRT: 205 AA.
ID IL6-ORC9C (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE 30-MAY-2000 (rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OC Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC NCBI_TaxID=9733;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Scott J.L., Perlick D.A.;
RA Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RA the killer whale (*Orcinus orca*) (Orcinus orca), and
RA Southern sea otter (*Phytocoryna litorea*).
RT Immunogenetics 43:190-195(1996).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELL DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO SUPERFAMILY

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CC

DR EMBL: L46803; AAB01429.1; -;
DR HSPF: P05231; 1AUU;
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin-6.
DR Pfam: PF00469; IL6.1;
DR PROSITE: PS00254; INTERLEUKIN-6.1.
KW Cytokine; glycoprotein; growth factor; signal.
FT SIGNAL 1 21
FT NON_TER 1
FT CHAIN 22 205 BY SIMILARITY.
FT DISULFID 64 170 INTERLEUKIN-6.
FT SIMILARITY 64 170 BY SIMILARITY.
FT CARBOHYD 164 164 N-GLYCOSYLATION. (POTENTIAL).
SO SEQUENCE 205 AA; 23366 MW; 630873A45760832 CR664.

Query Match

53.3%; Score 40; DB 1; Length 205;

Best Local Similarity 53.3%; Pred. No. 5.6;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 STRVLOPLOCKANN 15
DB 138 SSKALMLOPLOCKANN 152

RESULT 12

BIOF_AQOAE STANDARD; PRT: 373 AA.
ID BIOF_AQOAE
AC 066875;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DE 20-AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (AONS) (8-AMINO-7-
DE KETOPELARGONATE SYNTHASE) (7-KETO-8-AMINO-PELARGONIC ACID SYNTHETASE)
DE (7-KAP SYNTHETASE) (L-ALANINE-PIRUVYL COA LIGASE).
GN BIOF OR NO.626.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OC NCBI_TaxID=63503;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98156665; PubMed=9337320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.B., Marten P.V., Sheed M.A., Keller M., Aubay M., Huber R.,
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RT Nature 392:353-358(1998).

CC -1- CATALYTIC ACTIVITY: 6-CARBOXYHEXANOYL-COA + L-ALANINE -
CC 8-AMINO-7-OXONONANOATE + COA + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- PATHWAY: FIRST STEP IN BIOTIN BIOSYNTHESIS.
CC -1- FUNCTION: BELONGS TO CLASS-II OR PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AUTOTRANSFERASES

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CC

DR EMBL: AEO0669; AAC06836.1; -;
DR InterPro: IPR001917; Amiotransf.2.
DR Pfam: PF00222; amiotransf.2.1.
DR PROSITE: PS00599; AA_TRANSFR_CLASS.2.1.
KW Biotin biosynthesis; Transferrase; Pyridoxal phosphate;
KW Complete proteome. 223
SO SEQUENCE 373 AA; 42532 MW; 53638A505084401 CR664.

Query Match
Best Local Similarity 53.3%; Score 40; DB 1; Length 373;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 TYKLOPLOCKANN 16
DB 235 TKLLIDIVYKANKL 249

RESULT 13
E2E2_HUMAN STANDARD; PRT: 437 AA.
AC 014209;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DE 30-MAY-2000 (rel. 39, Last annotation update)

[illegible][illegible]

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: December 19, 2001, 16:25:18 (Search time 157.32 seconds
(without alignments))

14.876 Million cell updates/sec

Title: US-09-202-104A-2
Perfect score: 15
Sequence: 1 STKVLOFLQKRNKL 16
Scoring table: Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 14627329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPRENBL.17.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mollusc:*
8: sp.plant:*
9: sp.phage:*
10: sp.plant:*
11: sp.protein:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query	Match length	DB ID	Description
1	75	100.0	209	6	097540
2	60	80.0	175	6	097TH4
3	60	80.0	209	6	097TH4
4	50	66.7	207	6	097TH4
5	47	62.7	294	6	067775
6	47	62.7	294	6	067775
7	44	56.7	959	10	023281
8	44	56.7	1199	4	097439
9	42	56.0	286	5	097238
10	42	56.0	425	2	055879
11	42	56.0	517	10	097T05
12	42	56.0	822	10	023055
13	41	54.7	273	12	093657
14	41	54.7	273	12	093657
15	41	54.7	290	2	097402
16	40	53.3	75	12	097658
17	40	53.3	75	12	097658
18	40	53.3	75	12	097658
19	40	53.3	75	12	097658

Result	ID	Score	Query	Match length	DB ID	Description
1	097540	75	100.0	209	6	097540
2	097540	60	80.0	175	6	097TH4
3	097540	60	80.0	209	6	097TH4
4	097540	50	66.7	207	6	097TH4
5	097540	47	62.7	294	6	067775
6	097540	47	62.7	294	6	067775
7	097540	44	56.7	959	10	023281
8	097540	44	56.7	1199	4	097439
9	097540	42	56.0	286	5	097238
10	097540	42	56.0	425	2	055879
11	097540	42	56.0	517	10	097T05
12	097540	42	56.0	822	10	023055
13	097540	41	54.7	273	12	093657
14	097540	41	54.7	273	12	093657
15	097540	41	54.7	290	2	097402
16	097540	40	53.3	75	12	097658
17	097540	40	53.3	75	12	097658
18	097540	40	53.3	75	12	097658
19	097540	40	53.3	75	12	097658

ALIGNMENTS

Result	ID	Score	Query	Match length	DB ID	Description
1	097540	75	100.0	209	6	097540
2	097540	60	80.0	175	6	097TH4
3	097540	60	80.0	209	6	097TH4
4	097540	50	66.7	207	6	097TH4
5	097540	47	62.7	294	6	067775
6	097540	47	62.7	294	6	067775
7	097540	44	56.7	959	10	023281
8	097540	44	56.7	1199	4	097439
9	097540	42	56.0	286	5	097238
10	097540	42	56.0	425	2	055879
11	097540	42	56.0	517	10	097T05
12	097540	42	56.0	822	10	023055
13	097540	41	54.7	273	12	093657
14	097540	41	54.7	273	12	093657
15	097540	41	54.7	290	2	097402
16	097540	40	53.3	75	12	097658
17	097540	40	53.3	75	12	097658
18	097540	40	53.3	75	12	097658
19	097540	40	53.3	75	12	097658


```

RP SEQUENCE FROM N.A.
RP STRAIN-CV, COLUMBIA;
RA Theologis A., Osborne B.I., Vysotskaya V.S., Pederspiel N.A.,
RA Toriumi M., Yu G., Oji O., Araujo R., Chung E., Dewar K., Dietrich F.,
RA Becker J.R., Marshall A., Oeffner P., Davis R.W.;
RA Nucleotide (JAN-1997) to the EMBL/Genbank/DBS databases.
RP SEQUENCE FROM N.A.
RP STRAIN-CV, COLUMBIA;
RA Theologis A.;
RA Submitted (SEP-1997) to the EMBL/Genbank/DBS databases.
CC 1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
CC EMBL: AC000080; ANS7.DSAD
CC F000000000; ANS7.DSAD
DR Interpro: IPR000330; SMF2.N.
DR Interpro: IPR001841; ZNF-Finger.
DR Pfam: PF00097; ZF-CHRC4; 1.
DR Pfam: PF00097; ZF-CHRC4; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00487; RING; 1.
DR ZINC-Finger: ZINC00316; ZINC_FINGER_CHRC4; UNKNOWN_1.
SO SEQUENCE 822 AA; 92580 MW; ED4ED7DC97AC611 CRC64;

Query Match
Best Local Similarity 56.0%; Score 42; DB 10; Length 822;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 STKVLIQFIQKKRANL 16
    |||||:-:|||||
DB 220 STKVLYHGAKRKANL 235

RESULT 13
Q9KAZ2 PRELIMINARY; PRT; 75 AA.
AC Q9KAZ2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ORF1 (FRAGMENT).
OS RT virus.
OC Bacteriia; Filicutes; Bacillus/Clostridium group;
OC NCBI_TaxID=86887;
RN 1[1]_TaxID=68887;
RP SEQUENCE FROM N.A.
RA STRAIN-M129-5;
RA Utsuka H., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
RA Iizuka H., Miyakawa Y., Mayumi M.;
RT The entire nucleotide sequences of two distinct RT virus (TTV)
RT isolates (TUN01 and TUN02) remotely related to the original TTV
RT isolates (0-0-0/2000).
DR EMBL: AB028703; BA95912.1; -.
DR EMBL: AB028703; BA95912.1; -.
DR NON_TER 1
FT NON_TER 75
KW Complete proteins.
SQ SEQUENCE 75 AA; 8643 MW; 44A546A2PC94D0C8 CRC64;

Query Match
Best Local Similarity 54.7%; Score 41; DB 12; Length 75;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 STKVLIQFIQKKRANL 16
    |||||:-:|||||
DB 1 STKVLIQFIQKKRANL 16

RESULT 14
Q9JH26 PRELIMINARY; PRT; 264 AA.
AC Q9JH26;

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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ORF1 (FRAGMENT).
OS RT virus.
OC Bacteriia; Filicutes; Bacillus/Clostridium group;
OC NCBI_TaxID=86887;
RN 1[1]_TaxID=68887;
RP SEQUENCE FROM N.A.
RA STRAIN-M129-5;
RA Utsuka H., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
RA Iizuka H., Miyakawa Y., Mayumi M.;
RT The entire nucleotide sequences of two distinct RT virus (TTV)
RT isolates (TUN01 and TUN02) remotely related to the original TTV
RT isolates (0-0-0/2000).
DR Arch. Virol. 0-0-0/2000.
DR EMBL: AB028674; BA94883.1; -.
DR NON_TER 1
FT NON_TER 264
KW Complete proteins.
SQ SEQUENCE 264 AA; 31024 MW; BE35CA92A8B82E0F CRC64;

Query Match
Best Local Similarity 54.7%; Score 41; DB 12; Length 264;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 STKVLIQFIQKKRANL 16
    |||||:-:|||||
DB 190 STKVPTQFIQKKRANL 205

RESULT 15
Q9KAZ2 PRELIMINARY; PRT; 290 AA.
AC Q9KAZ2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE BH2194 PROTEIN.
OS Bacillus halodurans.
OC Bacteriia; Filicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OC NCBI_TaxID=86887;
RN 1[1]_TaxID=86887;
RP SEQUENCE FROM N.A.
RA STRAIN-C-125/JCM 9153;
RA MEDIANE-20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogawara N., Kubara S.,
RA Horikoshi K.;
RT Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.*;
DR EMBL: AB001514; BA805913.1; -.
DR EMBL: AB001514; BA805913.1; -.
DR NON_TER 1
FT NON_TER 290
KW Complete proteins.
SQ SEQUENCE 290 AA; 31713 MW; 8368C8B775M129 CRC64;

Query Match
Best Local Similarity 54.7%; Score 41; DB 2; Length 290;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RVLIQFIQKKRANL 14
    ||:-:|||||
DB 278 RVVSELIQKKRANL 289

Search completed: December 19, 2001, 16:25:19
Job time: 544 sec

```


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OM protein - protein search, using SW model

Run on: December 19, 2001, 16:20:58 (Search time 78.52 seconds
(without alignments)
4.585 Million cell updates/sec

Title: US-09-202-104A-2

Perfect score: 75

Sequence: 1 STKVLIOPILOKXKXKL 16

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database:

Issued Patents.AA:*

- 1: /cgn2.6/pdata/2/1aa/5A.COMB.pep:**
- 2: /cgn2.6/pdata/2/1aa/5B.COMB.pep:**
- 3: /cgn2.6/pdata/2/1aa/6A.COMB.pep:**
- 4: /cgn2.6/pdata/2/1aa/6B.COMB.pep:**
- 5: /cgn2.6/pdata/2/1aa/6C.COMB.pep:**
- 6: /cgn2.6/pdata/2/1aa/6D.COMB.pep:**

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	162	2	US-08-716-317-10
2	75	100.0	163	2	US-08-716-317-15
3	75	100.0	164	1	US-08-318-193-60
4	75	100.0	167	1	US-08-246-427A-2
5	75	100.0	167	2	US-08-766-620-2
6	75	100.0	172	2	US-08-919-101A-21
7	75	100.0	172	5	US-08-919-101A-20
8	75	100.0	172	5	US-08-149-101A-20
9	75	100.0	174	5	US-08-209-182C-4
10	75	100.0	181	1	US-08-209-182C-4
11	75	100.0	181	5	US-08-209-182C-4
12	75	100.0	181	5	US-08-209-182C-4
13	75	100.0	182	5	US-08-209-182C-4
14	75	100.0	183	1	US-08-209-182C-4
15	75	100.0	183	1	US-08-209-182C-4
16	75	100.0	184	1	US-08-567-047-2
17	75	100.0	184	2	US-08-567-047-2
18	75	100.0	184	2	US-08-567-047-2
19	75	100.0	184	2	US-08-567-047-2
20	75	100.0	184	2	US-08-567-047-2
21	75	100.0	184	2	US-08-567-047-2
22	75	100.0	184	2	US-08-567-047-2
23	75	100.0	184	2	US-08-567-047-2
24	75	100.0	184	2	US-08-567-047-2
25	75	100.0	184	2	US-08-567-047-2
26	75	100.0	184	2	US-08-567-047-2
27	75	100.0	184	2	US-08-567-047-2

SUMMARIES

28	75	100.0	185	1	US-07-918-181A-6
29	75	100.0	185	1	US-07-918-181A-8
30	75	100.0	185	1	US-08-231-575-2
31	75	100.0	185	1	US-08-231-575-6
32	75	100.0	185	1	US-08-231-575-6
33	75	100.0	185	1	US-08-231-575-6
34	75	100.0	185	1	US-08-246-427A-5
35	75	100.0	185	2	US-08-716-317-7
36	75	100.0	185	2	US-08-716-317-7
37	75	100.0	185	2	US-08-716-317-7
38	75	100.0	185	2	US-08-716-317-7
39	75	100.0	185	2	US-08-716-317-7
40	75	100.0	185	2	US-08-716-317-7
41	75	100.0	185	2	US-08-716-317-7
42	75	100.0	185	2	US-08-716-317-7
43	75	100.0	185	2	US-08-716-317-7
44	75	100.0	185	2	US-08-716-317-7
45	75	100.0	185	2	US-08-716-317-7

ALIGNMENTS

RESULT 1
US-08-716-317-10
: Sequence 10, Application 05/08716317
: Patent No. 5918654
: GENERAL INFORMATION:
: APPLICANT: TOSHIO HIDEKI
: APPLICANT: TOSHIO HIDEKI
: APPLICANT: TOSHIKAZU, HIROKO
: APPLICANT: NIKAI, HIROMICHI
: TITLE OF INVENTION: SECRETOR SIGNAL GENE AND EXPRESSION
: NUMBER OF SEQUENCES: 35
: NUMBER OF SEQUENCES: 35
: ADDRESS: OHLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIAN TYPE: Ploddy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-08/716-317
: FILING DATE: 02-07-1996
: PRIORITY DATA:
: APPLICATION NUMBER: PCT/JP96/00198
: FILING DATE: 01-FEB-1996
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: JP 17167/1995
: FILING DATE: 03-FEB-1996
: NAME: OHLON, NORMAN F.
: REGISTRATION NUMBER: 24,618
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INVENTOR: 10:
: LENGTH: 162 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein

US-08-716-317-10

Query Match 100.0%; Score 75; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STRVLI0PFI0KKAKNL 16
 DB 96 STRVLI0PFI0KKAKNL 111

RESULT 2

US-08-716-317-15
 ; Sequence 15, Application US/08716317
 ; Patent No. 5919654
 ; GENERAL INFORMATION:
 ; APPLICANT: YUKO
 ; APPLICANT: TOHMA, HIDEKI
 ; APPLICANT: TSUKAMOTO, HIROKO
 ; APPLICANT: NIKAGAI, KIYOKAZU
 ; APPLICANT: KIMAGAI, HIROMICHI
 ; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
 ; TITLE OF INVENTION: VECTOR CONTAINING IT
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSER: KOBLOM, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/716.317
 ; TELEPHONE: (703)936-9300
 ; TELEFAX: 899-453-4109
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP96/00198
 ; FILING DATE: 01-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 17167/1995
 ; FILING DATE: 03-FEB-1996
 ; NAME: GOSH, INOUE
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 59-924-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-716-317-15

Query Match 100.0%; Score 75; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STRVLI0PFI0KKAKNL 16
 DB 97 STRVLI0PFI0KKAKNL 112

RESULT 3
 US-08-318-193-60
 ; Sequence 60, Application US/08318193
 ; Patent No. 5641663
 ; GENERAL INFORMATION:
 ; APPLICANT: GARVIN, Robert T.
 ; APPLICANT: VALEK, Lawrence T.
 ; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
 ; OF PROTEINS
 ; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HEMATOLOGOUS
 ; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
 ; NUMBER OF SEQUENCES: 91
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSER: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA 22304
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/318.193
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935.314
 ; FILING DATE:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 18710/116 CACO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)936-9300
 ; TELEFAX: (703)963-4109
 ; INFORMATION FOR SEQ ID NO: 60:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 164 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-318-193-60

Query Match 100.0%; Score 75; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STRVLI0PFI0KKAKNL 16
 DB 98 STRVLI0PFI0KKAKNL 113

RESULT 4
 US-08-246-427A-2
 ; Sequence 2, Application US/08246427A
 ; Patent No. 5641657
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSEN, ET AL.
 ; TITLE OF INVENTION: Interleukin-6 Splice Variant
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSER: CARELLA, BYRNE, BAIN, GUTTFILIAN,
 ; ADDRESSER: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY


```

? COUNTRY: USA
? ZIP: 07068
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 INCH DISKETTE
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 2:
? STRANDS: CHAIN: 1
? LENGTH: 167 AMINO ACIDS
? TYPE: AMINO ACID
? STRANDEDNESS:
? TOPOLOGY: LINEAR
? MOLECULE TYPE: PROTEIN
US-08-766-620-2

? PRIOR APPLICATION DATA: 08/24/6, 427
? FILING DATE: MAY 19, 1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: FERRARO, GREGORY D.
? REGISTRATION NUMBER: 36,134
? REFERENCE/DOCKET NUMBER: 325800-
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 167 AMINO ACIDS
? TYPE: AMINO ACID
? STRANDEDNESS: LINEAR
? TOPOLOGY: LINEAR
? MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match
Best Local Similarity 100.0%; Score 75; DB 1; Length 167;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVLIQFLOKKANL 16
|||||
DB 101 STVLIQFLOKKANL 116

RESULT
5
US-08-766-620-2
? Sequence 2, Application US/08766620
? Patent No 5058400
? GENERAL INFORMATION:
? APPLICANT: ROSEN, ET AL.
? TITLE OF INVENTION: Interleukin-6 Splice Variant
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
? ADDRESS: 6 BECKER FARM ROAD
? STREET: 6 BECKER FARM ROAD
? CITY: ROSELAND
? STATE: NEW JERSEY
? COUNTRY: USA
? ZIP: 07068
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 INCH DISKETTE
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: WORD PERFECT 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/766, 620
? FILING DATE: December 12, 1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/246, 427
? FILING DATE: MAY 19, 1994
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: MULLINS, J G.
? REGISTRATION NUMBER: 33, 073

```

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? REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 2:
? STRANDS: CHAIN: 1
? LENGTH: 167 AMINO ACIDS
? TYPE: AMINO ACID
? STRANDEDNESS:
? TOPOLOGY: LINEAR
? MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match
Best Local Similarity 100.0%; Score 75; DB 2; Length 167;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVLIQFLOKKANL 16
|||||
DB 101 STVLIQFLOKKANL 116

RESULT
6
PCT-US95-06094-2
? Sequence 2, Application PC/TUS9506094
? GENERAL INFORMATION:
? APPLICANT: ROSEN, ET AL.
? TITLE OF INVENTION: Interleukin-6 Splice Variant
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
? ADDRESS: 6 BECKER FARM ROAD
? STREET: 6 BECKER FARM ROAD
? CITY: ROSELAND
? STATE: NEW JERSEY
? COUNTRY: USA
? ZIP: 07068
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 INCH DISKETTE
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: WORD PERFECT 5.1
? CURRENT APPLICATION DATA: PCY/US95/06094
? FILING DATE: Submitted herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/246, 427
? FILING DATE: MAY 19, 1994
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? ADDRESS: 6 BECKER FARM ROAD
? STREET: 6 BECKER FARM ROAD
? CITY: ROSELAND
? STATE: NEW JERSEY
? COUNTRY: USA
? ZIP: 07068
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 2:
? STRANDS: CHAIN: 1
? LENGTH: 167 AMINO ACIDS
? TYPE: AMINO ACID
? STRANDEDNESS:
? TOPOLOGY: LINEAR
? MOLECULE TYPE: PROTEIN
PCT-US95-06094-2

Query Match
Best Local Similarity 100.0%; Score 75; DB 5; Length 167;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVLIQFLOKKANL 16

```

DB 101 STKVLIQFLOKKAKML 116

RESULT 7

US-08-149-101A-21
Sequence 21, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD FOR WINDOWS

CLASSIFICATION: 530

APPLICATION NUMBER: US/08/149-101A

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION: and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEFAX: (206)282-7100

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1172

TYPE: amino acid

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE: no

ORIGINAL SOURCE:

ORGANISM: homo sapien

US-08-149-101A-21

Query Match 100.0%; Score 75; DB 4; Length 172;

Best Local Similarity 100.0%; Fred No. 5,7e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKKAKML 116

DB 119 STKVLIQFLOKKAKML 134

RESULT 8

Sequence 21, Application PC/TUS9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD FOR WINDOWS

CURRENT APPLICATION DATA: PCT/US94/12873

APPLICATION NUMBER: PCT/US94/12873

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1172

TYPE: amino acid

MOLECULE TYPE: linear

PCF-US94-12873-21

Query Match 100.0%; Score 75; DB 5; Length 172;

Best Local Similarity 100.0%; Fred No. 5,7e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKKAKML 116

DB 119 STKVLIQFLOKKAKML 134

RESULT 9

US-08-149-101A-20

Sequence 20, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD FOR WINDOWS

CURRENT APPLICATION DATA: US/08/149-101A

APPLICATION NUMBER: 32,585 and 36,131, respectively

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Oser, Jeffrey B. and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEFAX: (206)282-7100

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1174

TYPE: amino acid

MOLECULE TYPE: linear

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE: no

ORIGINAL SOURCE:

ORGANISM: homo sapien

US-08-149-101A-20

Query Match 100.0%; Score 75; DB 4; Length 174;
 Best Local Similarity 100.0%; Pctd. No. 5, 8e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKYLIQFLOKRAKRL 16
 Db 119 STKYLIQFLOKRAKRL 134

RESULT 10
 PCT-US94-12873-20
 Sequence 20 Application PC/TUS9412873
 GENERAL INFORMATION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TITLE OF INVENTION: HYBRID CYTOKINES
 NUMBER OF SEQUENCES: 20
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
 COMPUTER: AST-IBM Compatible
 OPERATING SYSTEM: MS-DOS Version 6
 SOFTWARE: WORD FOR WINDOWS
 CURRENT APPLICATION DATA:
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US94-12873-20

Query Match 100.0%; Score 75; DB 5; Length 174;
 Best Local Similarity 100.0%; Pctd. No. 5, 8e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKYLIQFLOKRAKRL 16
 Db 119 STKYLIQFLOKRAKRL 134

RESULT 11
 US-08-209-182C-4
 Sequence 4 Application US/08209182C
 Patent No. 5545537
 GENERAL INFORMATION:
 APPLICANT: Skelly, Susan M.
 APPLICANT: Jackney, Charles T.
 APPLICANT: Snouwaert, John N.
 APPLICANT: Fowlkes, Dana M.
 TITLE OF INVENTION: Cysteine Depleted IL-6 Mutains
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Imclone Systems Incorporated
 STREET: 180 Varick Street
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10014
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 10-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/724,698
 FILING DATE: 02-JUL-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Felt, Irving N.
 REGISTRATION NUMBER: 28,601
 REFERENCE/DOCKET NUMBER: SRE-1-PD
 TELEPHONE: 212-645-1405
 TELEFAX: 212-645-2054
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-209-182C-4

Query Match 100.0%; Score 75; DB 1; Length 181;
 Best Local Similarity 100.0%; Pctd. No. 6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKYLIQFLOKRAKRL 16
 Db 115 STKYLIQFLOKRAKRL 130

RESULT 12
 PCT-US92-05612-4
 Sequence 4 Application PC/TUS9205612
 GENERAL INFORMATION:
 APPLICANT: Skelly, Susan M.
 APPLICANT: Jackney, Charles T.
 APPLICANT: Snouwaert, John N.
 APPLICANT: Fowlkes, Dana M.
 TITLE OF INVENTION: Cysteine Depleted IL-6 Mutains
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Imclone Systems Incorporated
 STREET: 180 Varick Street
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10014
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 19920702
 APPLICATION NUMBER: PCT/US92/05612
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: N. 28,601
 REFERENCE/DOCKET NUMBER: SRE-1-PD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-645-1405
 TELEFAX: 212-645-2054
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US92-05612-4

Query Match 100.0%; Score 75; DB 5; Length 181;
 Best Local Similarity 100.0%; Pctd. No. 6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKYLIQFLOKRAKRL 16

DB 115 STRKVLQFLOKXKAKNL 130

RESULT 13

US-08-149-101A-25

Sequence 25, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Leung, David W.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44MB, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149-101A

FILING DATE: 8-NO. 6171824-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/097,869

FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: US/08/149-101A and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 01058

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)282-6206

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1182

TYPE: amino acid

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORGANISM: Homo sapien

US-08-149-101A-25

Query Match 100.0%; Score 75; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 6,1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STRKVLQFLOKXKAKNL 16

|||||

DB 119 STRKVLQFLOKXKAKNL 134

RESULT 14

PC-US94-12873-25

Sequence 25, Application PC/US9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44MB, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC/US9412873

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 182

TYPE: amino acid

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORGANISM: Homo sapien

US-08-009-973-1

Query Match 100.0%; Score 75; DB 5; Length 182;

Best Local Similarity 100.0%; Pred. No. 6,1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STRKVLQFLOKXKAKNL 16

|||||

DB 117 STRKVLQFLOKXKAKNL 132

RESULT 15

US-08-009-973-1

Sequence 1, Application US/08009973

Patent No. 5338834

GENERAL INFORMATION:

APPLICANT: WILLIAMS, Ashley M.

TITLE OF INVENTION: Ultrapure Human Interleukin-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Polysciences

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009,973

FILING DATE: 19930126

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/199 ALLE

TELECOMMUNICATION INFORMATION:

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 183 amino acids

TYPE: AMINO ACID

MOLECULE TYPE: linear

US-08-009-973-1

Query Match 100.0%; Score 75; DB 1; Length 183;

Best Local Similarity 100.0%; Pred. No. 6,1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STRKVLQFLOKXKAKNL 16

|||||

DB 117 STRKVLQFLOKXKAKNL 132

Search completed: December 19, 2001, 16:20:58

Job time: 403 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:33 ; Search time 170.68 Seconds
(without alignments)
8.246 Million cell updates/sec

File: us-09-202-104a-3

Perfect score: 1 IIRSRKRFQSSIRALQM 19

Sequence: BLOSUM62

Gapop 10.0, Gapext 0.5

Scoring table: 522463 seqs, 7407390 residues

Searched: 522463 seqs, 7407390 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

Database	Score	Match	Length	DB	ID	Description
1: /SIDSR/9cgdata/geneseq/AA1980.DAT:*	88	100.0	19	19	AA052203	Interleukin-6 anka
2: /SIDSR/9cgdata/geneseq/AA1981.DAT:*	88	100.0	65	17	AA004402	Interleukin-6 anka
3: /SIDSR/9cgdata/geneseq/AA1982.DAT:*	88	100.0	148	22	AA002910	Angiotensin conver
4: /SIDSR/9cgdata/geneseq/AA1983.DAT:*	88	100.0	151	16	AA077393	Human mutant IL-6a
5: /SIDSR/9cgdata/geneseq/AA1984.DAT:*	88	100.0	151	16	AA077393	Human mutant IL-6a
6: /SIDSR/9cgdata/geneseq/AA1985.DAT:*	88	100.0	162	17	AA000131	Human interleukin-
7: /SIDSR/9cgdata/geneseq/AA1986.DAT:*	88	100.0	162	17	AA000131	Human interleukin-
8: /SIDSR/9cgdata/geneseq/AA1987.DAT:*	88	100.0	166	16	AA077393	Human interleukin-
9: /SIDSR/9cgdata/geneseq/AA1988.DAT:*	88	100.0	167	17	AA077393	Human interleukin-
10: /SIDSR/9cgdata/geneseq/AA1989.DAT:*	88	100.0	169	16	AA077387	Human IL-6 mutant

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	ID	AA052203	standard; peptide: 19 AA.	ALIGNMENTS
1	AA052203;	09-JUN-1998	(first entry)	Interleukin-6 antagonist peptide.
2	AA052203;	09-JUN-1998	(first entry)	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma; acquired immune deficiency syndrome-related lymphoma; immune response; rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy; Alzheimer's disease.
3	AA052203;	09-JUN-1998	(first entry)	Synthetic.
4	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
5	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
6	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
7	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
8	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
9	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
10	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
11	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
12	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
13	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
14	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
15	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
16	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
17	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
18	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
19	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
20	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
21	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
22	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
23	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
24	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
25	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
26	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
27	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
28	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
29	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
30	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
31	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
32	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
33	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
34	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
35	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
36	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
37	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
38	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
39	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
40	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
41	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
42	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
43	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
44	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.
45	AA052203;	09-JUN-1998	(first entry)	Hom sapiens.

New peptide(s) with interleukin-6 agonist or antagonist activity -
useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 PS Claim 6; Page 17: 28pp; English.
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6-related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome, Alzheimer's disease etc.) also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and thus they are not immunogenic. They are not
 CC suitable for any therapy nor toxic for polymorphonuclear cells or
 CC hepatocytes). contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 CC Sequence 19 AA:
 SQ
 Query Match 100.0%; Score 88; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 IIRSEKFEKLOSSIRALRQM 19
 Db 1 IIRSEKFEKLOSSIRALRQM 19
 RESULT 2
 AAAM00402 standard; peptide: 65 AA.
 ID AAAM00402:
 XX
 XX
 XX 29-AUG-1996 (first entry)
 DT
 DE Interleukin-6 antagonist peptide.
 KW IL-6; antagonist; autoimmune disease.
 XX
 XX Synthetic.
 XX
 XX JF07324097-A.
 PM
 XX 12-DEC-1995.
 PD
 XX 30-MAY-1994; 94AP-0117259.
 PP
 XX 30-MAY-1994; 94AP-0117259.
 XX
 XX (DAI) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 XX WPI: 1996-065476/07.
 DR
 XX Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 XX Claim 1; Page 2; 19pp; Japanese.
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAAM00401, AAAM00402 (the present sequence), AAAM00403
 CC or AAAM00404, where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAAM00401-404) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 CC
 CC Sequence 65 AA:
 SQ
 Query Match 100.0%; Score 88; DB 17; Length 65;
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 IIRSEKFEKLOSSIRALRQM 19
 Db 47 IIRSEKFEKLOSSIRALRQM 65
 RESULT 3
 AAAM002910 standard; protein: 148 AA.
 ID AAAM002910:
 XX
 XX 12-SEP-2001 (first entry)
 DT
 DE Angiotensin converting enzyme (ACEV) splice variant protein #10.
 XX
 XX
 XX Angiotensin converting enzyme (ACEV) splice variant; interleukin 6;
 KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KW platelet-derived endothelial cell growth factor; cardiovascular disease;
 KW cellular tumour antigen p53; cyclin-dependent kinase/sclerosis; cancer;
 KW nasopharyngeal infection; postnatal arterial thrombosis; renal disease;
 KW metabolic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KW nonrheumatic pulmonary granulomatous disease; endothelial abnormality;
 KW vascular disorder; asbestosis.
 KW
 XX Homo sapiens.
 OS
 XX
 XX M0200136632-A2.
 XX
 XX 25-MAY-2001.
 PD
 XX 17-NOV-2000; 2000MO-1140766.
 PP
 XX 17-NOV-1999; 99IL-0132878.
 XX 10-DEC-1999; 99IL-0133455.
 XX
 XX (COMP-) COMPTGEN LTD.
 PA
 XX
 XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 PI
 XX WPI: 2001-336004/35.
 DR
 XX N-PSDB: AAS06010.
 XX
 XX Novel alternative splicing variants e.g. variant of angiotensin
 PP converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies
 XX
 XX Claim 4; Fig 10; 51pp; English.
 BS
 XX The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) peptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1c, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding to the variant and diagnosis of
 CC the variant. The variant is useful for the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,

CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonautoimmune pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.

SO Sequence 148 AA:

Query Match 100.0%; Score 88; DB 22; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1,3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIRSRKFEFGSSLRALROM 19
 DB 130 IIRSRKFEFGSSLRALROM 148

RESULT 4

AA077393
 ID AA077393 standard; Protein: 151 AA.

AA077393:

17-APR-1996 (first entry)

Human mutant IL-6α/C3 (amino acids 5-19, 44-50 and 73-83 deleted).

Human interleukin-6; IL-6α/C3 mutant; Increased stability;

recombinant; production; deletion mutant;

amino acids 5-19, 44-50 and 73-83.

Homo sapiens.

JF07224097-A.

22-AUG-1995.

08-FEB-1994; 94JP-0014461.

08-FEB-1994; 94JP-0014461.

(ASNG) ASAHI GLASS CO LTD.

WPI: 1995-325556/42.

N-PSDB: AA094347.

Interleukin-6 mutant, related DNA and expression vectors - has

higher stability than natural interleukin-6

Claim 1: Pages 15-16; 18pp; Japanese.

AA094348 encodes AA077393 the human IL-6 deletion mutant IL-6α/C3

which lacks the amino acids Gly5-Leu19, Cys44-Cys50 and Cys73-Cys83

of the wild type protein. The cDNA can be used for the recombinant

prodn. of IL-6α/C3 which has increased stability compared to wild

type IL-6.

Sequence 151 AA:

Query Match 100.0%; Score 88; DB 16; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1,3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIRSRKFEFGSSLRALROM 19
 DB 133 IIRSRKFEFGSSLRALROM 151

RESULT 5

AA077392

AA077392 standard; Protein: 158 AA.

AA077392:

17-APR-1996 (first entry)

Human mutant IL-6α/C2 (amino acids 5-19 and 73-83 deleted).

Human interleukin-6; IL-6α/C2 mutant; Increased stability;

recombinant; production; deletion mutant;

amino acids 5-19 and 73-83.

Homo sapiens.

JF07224097-A.

22-AUG-1995.

08-FEB-1994; 94JP-0014461.

08-FEB-1994; 94JP-0014461.

(ASNG) ASAHI GLASS CO LTD.

WPI: 1995-325556/42.

N-PSDB: AA094347.

Interleukin-6 mutant, related DNA and expression vectors - has

higher stability than natural interleukin-6

Claim 1: Pages 14-15; 18pp; Japanese.

AA094347 encodes AA077392 the human IL-6 deletion mutant IL-6α/C2

which lacks the amino acids Gly5-Leu19 and Cys73-Cys83 of the

wild type protein. The cDNA can be used for the recombinant prodn.

of IL-6α/C2 which has increased stability compared to wild type

IL-6.

Sequence 158 AA:

Query Match 100.0%; Score 88; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1,3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIRSRKFEFGSSLRALROM 19
 DB 140 IIRSRKFEFGSSLRALROM 158

RESULT 6

AA077391

AA077391 standard; Protein: 162 AA.

AA077391:

17-APR-1996 (first entry)

Human mutant IL-6α/C1 (amino acids 5-19 and 44-50 deleted).

Human interleukin-6; IL-6α/C1 mutant; Increased stability;

recombinant; production; deletion mutant;

amino acids 5-19 and 44-50.

Homo sapiens.

JF07224097-A.

22-AUG-1995.

```

XX 08-FEB-1994; 94JJP-001461.
XX animal cell viral promoter; sequence of a hIL-6 fragment, 162
XX 08-FEB-1994; 94JJP-001461.
XX (ASAC ) ASAH1 GLASS CO LTD.
XX WPI: 1996-325556/42.
XX N-PSDB; AA094346.
XX Interleukin-6 mutant, related DNA and expression vectors - has
XX higher stability than natural Interleukin-6
XX Claim 1; Page 14; 18pp; Japanese.
XX AA094346 encodes AAR7391 the human IL-6 deletion mutant IL-6a/Cl,
XX which lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the
XX wild type protein. The cDNA can be used for the recombinant protein
XX IL-6a/Cl, which has increased stability compared to wild type
XX IL-6.
XX Sequence 162 AA:
SO
Query Match 100.0%; Score 88; DB 16; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 IIRSFKEFLSSIRALROM 19
Db 144 IIRSFKEFLSSIRALrgm 162
RESULT 7
ID AA00131 standard; Protein: 162 AA.
AC AA00131;
XX 09-APR-1997 (first entry)
XX Human Interleukin-6 fragment.
XX Secretory; signal peptide; P-factor; multicloning vector; PCR;
XX animal protein; expression; production; recombinant; primer;
XX fission yeast; human; serum albumin; Interleukin-6;
XX polymerase chain reaction; Schizosaccharomyces pombe;
XX PO fragment.
XX Homo sapiens.
XX WO6623890-A1.
XX 08-AUG-1996.
XX 96WO-JF00138.
XX 01-FEB-1996; 96WO-JF00138.
XX 03-FEB-1995; 95JP-0017167.
XX (ASAC ) ASAH1 GLASS CO LTD.
XX Hama Y., Kumagai H., Nakai K., Tohda H., Tsukamoto H.;
XX WPI: 1996-371438/37.
XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
XX cDNA, a Schizosaccharomyces pombe secretory signal peptide
XX - for production of vectors for expression of animal proteins in a
XX fission yeast, pref. S. pombe, host
XX Example 4; Pages 28-29; 50pp; Japanese.
XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
XX cDNA, a Schizosaccharomyces pombe secretory signal peptide
XX

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CC fragment or P-factor fragment (PO fragment) DNA and preferably an
CC animal cell viral promoter; sequence of a hIL-6 fragment, 162
CC 08-FEB-1994; 94JJP-001461.
CC the present sequence, in a fission yeast host, preferably S. pombe,
CC culture.
XX Sequence 162 AA:
SO
Query Match 100.0%; Score 88; DB 17; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 IIRSFKEFLSSIRALROM 19
Db 144 IIRSFKEFLSSIRALrgm 162
RESULT 8
ID AA00132 standard; Protein: 163 AA.
AC AA00132;
XX 09-APR-1997 (first entry)
XX Human Interleukin-6 fragment.
XX Secretory; signal peptide; P-factor; multicloning vector; PCR;
XX animal protein; expression; production; recombinant; primer;
XX fission yeast; human; serum albumin; Interleukin-6;
XX polymerase chain reaction; Schizosaccharomyces pombe;
XX PO fragment.
XX Homo sapiens.
XX WO6623890-A1.
XX 08-AUG-1996.
XX 96WO-JF00138.
XX 01-FEB-1996; 96WO-JF00138.
XX 03-FEB-1995; 95JP-0017167.
XX (ASAC ) ASAH1 GLASS CO LTD.
XX Hama Y., Kumagai H., Nakai K., Tohda H., Tsukamoto H.;
XX WPI: 1996-371438/37.
XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
XX cDNA, a Schizosaccharomyces pombe secretory signal peptide
XX - for production of vectors for expression of animal proteins in a
XX fission yeast, pref. S. pombe, host
XX Example 7; Pages 30-31; 50pp; Japanese.
XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
XX cDNA, a Schizosaccharomyces pombe secretory signal peptide
XX fragment or P-factor fragment (PI fragment) DNA and preferably an
XX animal cell viral promoter sequence and a neomycin resistance gene,
XX can be used for the efficient production of a hIL-6 fragment, i.e.
XX the present sequence, in a fission yeast host, preferably S. pombe,
XX culture.
XX Sequence 163 AA:
SO
Query Match 100.0%; Score 88; DB 17; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 IIRSFKEFLSSIRALROM 19

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Db 145 ilrskfqlgsalrqlgm 163

RESULT 9

AA077390 ID AAR77390 standard; Protein: 166 AA.

AC AAR77390:

XX 17-APR-1996 (first entry)

XX

XX Human IL-6 mutant IL-6C3 (amino acids 44-50 and 73-83 deleted).

XX Human Interleukin-6; IL-6C3 mutant; Increased stability;

XX recombinant; production; deletion mutant;

XX amino acids 44-50 and 73-83.

XX Homo sapiens.

XX Key location/Qualifiers

XX mlt_peptide 1:498

XX FT /*tag= a

XX JP07224097-A.

XX

XX 22-AUG-1995.

XX

XX 08-FEB-1994: 94JP-0014461.

XX

XX 08-FEB-1994: 94JP-0014461.

XX

XX (ASAC) ASAH1 GLASS CO LTD.

XX PA

XX WPI: 1995-325556/42.

XX DR

XX N-PSDB: AA094345.

XX

XX Interleukin-6 mutant; related DNA and expression vectors - has

XX higher stability than natural Interleukin-6

XX

XX Claim 1: Page 13: 18pp: Japanese.

XX PS

XX AA094345 encodes AAR77390 the human IL-6 deletion mutant IL-6C3,

XX which lacks the amino acids Cys44-Cys50 and Cys73-Cys83 of the

XX CC natural protein. The protein is recombinant, produced by the

XX CC expression of IL-6C3, which has increased stability compared to wild type

XX IL-6.

XX

XX Sequence 166 AA:

XX

Query Match 100.0%; Score 88; DB 16; Length 166;

Best Local Similarity 100.0%; Pred. No. 1,4e+06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALRQM 19

DB 148 ilrskfqlgsalrqlgm 166

RESULT 10

AA077649 ID AAR77649 standard; Protein: 167 AA.

AC AAR77649:

XX 27-JUN-1996 (first entry)

XX

XX Human Interleukin-6 splice variant.

XX

XX Human; Interleukin-6; splice variant; IL-6SV; treatment;

XX immunotherapeutic; anti-inflammatory; bone marrow transplant;

XX chemotherapy; side effect; corneal damage; keratitis; ulcer;

XX antagonist; Castleman's disease; multiple myeloma;

XX

KW cardiac myoma; cervical cancer; rheumatoid arthritis;

KW autoimmune diabetes; sepsis.

XX

XX Homo sapiens.

XX

XX MO9532282-A1.

XX

XX 30-NOV-1995.

XX

XX 17-MAY-1995: 95MO-US06094.

XX

XX 19-MAY-1994: 94US-0246427.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX PA

XX Adams MD, LI H, Ruben S;

XX

XX WPI: 1996-020577/02.

XX DR

XX N-PSDB: AAT08558.

XX

XX Polynucleotide encoding interleukin-6-splice variant - used for

XX treating auto-immune diseases and inflammation.

XX

XX Claim 1: Page 40: 54pp: English.

XX PS

XX The human Interleukin-6 splice variant (IL-6SV) AAR77649 is encoded

XX CC by AAT08558 (which is derived from an activated macrophage cDNA

XX CC library), and may be used in immunotherapeutic and

XX CC immunotherapeutic purposes in the treatment of patients

XX CC suffering from bone marrow transplant chemotherapy side effects,

XX CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may

XX CC be used to treat diseases caused by the up-regulated prodn. of

XX CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myoma,

XX CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),

XX CC and sepsis.

XX

XX Sequence 167 AA:

XX

Query Match 100.0%; Score 88; DB 17; Length 167;

Best Local Similarity 100.0%; Pred. No. 1,4e+06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALRQM 19

DB 149 ilrskfqlgsalrqlgm 167

RESULT 11

AAR77387 ID AAR77387 standard; Protein: 169 AA.

AC AAR77387:

XX 17-APR-1996 (first entry)

XX

XX Human IL-6 mutant IL-6a (amino acids 5-19 deleted).

XX

XX Human Interleukin-6; IL-6a mutant; Increased stability;

XX recombinant; production; deletion mutant; amino acids 5-19.

XX

XX Homo sapiens.

XX

XX JF07224097-A.

XX PN

XX 22-AUG-1995.

XX

XX 08-FEB-1994: 94JP-0014461.

XX

XX 08-FEB-1994: 94JP-0014461.

XX

XX (ASAC) ASAH1 GLASS CO LTD.

XX PA

DR WPI: 1995-325556/42.
 DR N-PSDB: AAO94342.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 XX
 PS Claim 1: Page 10: 18pp: Japanese.
 CC AAO94342 encodes AAR7387 the human IL-6 deletion mutant IL-6a, which
 CC lacks the amino acids Gly5-Leu15 of the wild type protein. The
 CC cDNA can be used for the recombinant prodn. of IL-6a, which has
 CC increased stability compared to wild type IL-6.
 XX
 SQ Sequence 169 AA:
 Query Match 100.0%; Score 88; DB 16; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ILRSFKFEILOSSIRALRQW 19
 Db 151 ILRSFKFEIqgsIRalrqp 169
 RESULT 12
 AAR7388
 ID AAR7389 standard: Protein: 173 AA.
 XX AAR7389;
 AC AAR7389;
 XX
 DT 17-APR-1996 (first entry)
 XX
 XX Human IL-6 mutant IL-6C2 (amino acids 73-83 deleted).
 XX Human Interleukin-6; IL-6C2 mutant; increased stability;
 KM recombinant; production; deletion mutant; amino acids 73-83.
 XX
 OS Homo sapiens.
 XX
 XX Key: Location/Qualifiers
 XX mat_peptide 1..519
 XX /tag= a
 XX
 FN JP07224097-A.
 XX
 XX 22-AUG-1995.
 PD
 XX 08-FEB-1994: 94JP-0014461.
 XX
 PR 08-FEB-1994: 94JP-0014461.
 XX
 PA (ASAC) ASAHI GLASS CO LTD.
 XX
 XX WPI: 1995-325556/42.
 XX N-PSDB: AAO94344.
 DR
 XX
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 XX
 PS Claim 1: Page 12: 18pp: Japanese.
 CC AAO94344 encodes AAR7389 the human IL-6 deletion mutant IL-6C2,
 CC which lacks the amino acids Gly5-Leu15 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
 CC has increased stability compared to wild type IL-6.
 XX
 SQ Sequence 173 AA:
 Query Match 100.0%; Score 88; DB 16; Length 173;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILRSFKFEILOSSIRALRQW 19
 Db 155 ILRSFKFEIqgsIRalrqp 173
 RESULT 13
 AAR7388
 ID AAR7389 standard: Protein: 177 AA.
 XX AAR7389;
 AC AAR7389;
 XX
 DT 17-APR-1996 (first entry)
 XX
 XX Human IL-6 mutant IL-6C1 (amino acids 44-50 deleted).
 DE Human Interleukin-6; IL-6C1 mutant; increased stability;
 KM recombinant; production; deletion mutant; amino acids 44-50.
 XX
 OS Homo sapiens.
 XX
 FN JP07224097-A.
 XX
 XX 22-AUG-1995.
 PD
 XX 08-FEB-1994: 94JP-0014461.
 XX
 PR 08-FEB-1994: 94JP-0014461.
 XX
 PA (ASAC) ASAHI GLASS CO LTD.
 XX
 XX WPI: 1995-325556/42.
 XX N-PSDB: AAO94343.
 DR
 XX
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 XX
 PS Claim 1: Page 11: 18pp: Japanese.
 CC AAO94343 encodes AAR7388 the human IL-6 deletion mutant IL-6C1,
 CC which lacks the amino acids Gly5-Leu15 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C1, which
 CC has increased stability compared to wild type IL-6.
 XX
 SQ Sequence 177 AA:
 Query Match 100.0%; Score 89; DB 16; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ILRSFKFEILOSSIRALRQW 19
 Db 159 ILRSFKFEIqgsIRalrqp 177
 RESULT 14
 AAR7334
 ID AAR7334 standard: Protein: 179 AA.
 XX
 AC AAR7334;
 XX
 XX 13-DEC-1995 (first entry)
 DT
 XX
 XX Human Interleukin-6 (IL-6).
 DE Human Interleukin-6 (IL-6).
 XX
 KM Cytokine; tumour proliferation; cancer therapy.
 XX
 OS Homo sapiens.
 XX
 XX W05513393-A.
 XX
 PD 18-MAY-1995.

XX	PP	07-NOV-1994:	94NO-USL2873.
XX	XX	08-NOV-1993:	93NO-U0149101.
PA	PA	(HUTC-) HUTCHINSON CANCER RES CENTER FRED.	
XX	XX	Leung DM, Rose TM, Todaro GJ:	
PI	XX	WPI; 1995-184111/25.	
DR	XX	NPSDB; AAO87153.	
PT	PT	New hybrid cytokines with alpha helical sequences from different	
PT	PT	sources - also cDNA encoding them, vectors and transformed cells,	
PT	PT	useful e.g. for treating cancer, remodelling bone etc.	
XX	XX	Disclosure: Page 23-24; 52pp; English.	
XX	XX	The cytokine encoding genes for leukemia inhibitory factor (LIF),	
CC	CC	gamma-interferon-inducing factor (GIF), interleukin-6 (IL-6),	
CC	CC	transforming growth factor-beta type I (TGF-beta1) and osteostatin-	
CC	CC	monoclonal antibody (OSM) have been cloned and reported in the literature.	
CC	CC	IL-6, G-CSF, LIF, IL-11, CDFP and OSM each comprise four alpha-	
CC	CC	helical sequences. In each cytokine, the four alpha-helical	
CC	CC	sequences are linked by non-alpha-helical 'linking' sequences of	
CC	CC	about 5-100 Aas, and in some cases the alpha-helices are maintained	
CC	CC	in the proper conformation and geometry with respect to each other	
CC	CC	through disulfide bridges. The invention provides a group of	
CC	CC	about 10 kDa. Each hybrid cytokine comprises three or four	
CC	CC	alpha-helical sequences and linking sequences, ranging from about	
CC	CC	5-40 Aas in length, selected from the linking sequences of the	
XX	XX	above cytokines or other linking sequences.	
SQ	SQ	Sequence 179 AA:	
XX	XX	Sequence 179 AA:	
Query Match		Score 88; DB 16; Length 179;	
Best Local Similarity	100.0%;	Pred. No. 1,5e-06;	
Matches 19:	Conservative 0;	Mismatches 0;	Gaps 0;
OY		1 ILRSKFETQSSIRALROM 19	
Db		161 ILRSKELIGSISIRALrgm 179	
RESULT 15			
AAR31996		AAR31996 standard; Protein: 181 AA.	
ID			
AC	AA	AAR31996;	
XN	XN	07-JUN-1993 (first entry)	
DM	DM	-4aa IL-6 SSSS mutcin.	
XX	XX		
DE	DE	Interleukin-6; mutant protein; pgaI/EK/cEU-6.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
FM	FM	Key Location/Qualifiers	
FT	FT	Misc-difference 41 /note= "ser replaces wild-type Cys"	
FT	FT	Misc-difference 47 /note= "ser replaces wild-type Cys"	
FT	FT	Misc-difference 70 /note= "ser replaces wild-type Cys"	
FT	FT	Misc-difference 70 /note= "ser replaces wild-type Cys"	
XX	XX	/note= "set replaces wild-type Cys"	
XX	XX	MO9301212-A.	
XX	XX	21-JAN-1993.	

XX	02-JUL-1992:	92WO-US05612.
XX		
XX	02-JUL-1991:	91US-0724698.
XX		
XX	(IMC-) IMCONE SYSTEMS, INC.	
XX	(UYNC-) UNIV NORTH CAROLINA.	
XX		
PI	FOWLES DM, Skelly SM, Snowaert JN, Tackney CF;	
DR	WEI: 1993-045433/05.	
XX		
DR	N-PSDB: ABO34345.	
XX		
PI	New cysteine-depleted Interleukin-6 mutin - for promoting cell	
PI	differentiation (e.g. of B-cells), as antiinflammatory agents and	
PI	for treating thrombocytopaenia	
XX		
XX	Example 1; Fig 2; 118pp; English.	
XX		
XX	plasmid pB9a1/EK/cfll-6 contains a DNA sequence which encodes a	
XX	full-length mature IL-6 protein having a sequence identical to the	
XX	full-length mature IL-6 protein having a sequence identical to the	
XX	interleukin-6 cleavage site, which is, in turn, followed by a	
XX	synthetic IL-6 peptide sequence. The IL-6 mutin sequence is that of	
XX	of native IL-6 except that the four cysteine residues, which occur	
XX	at positions 45, 51, 74 and 84 of the mature full-length IL-6	
XX	molecule are replaced by serine residues. A truncated 0.58kb	
XX	cysteine free IL-6 sequence lacking the first 4 N-terminal amino	
XX	acids can be isolated by EcoRI/HindIII digestion. The fragment was	
XX	then ligated into the pB9a1 vector. The resulting recombinant	
XX	or N-terminally truncated, IL-6 was found that restoring the last 4	
XX	Cys residues (at positions 74 and 84) resulted in a mutin which	
XX	retained IL-6 activity.	
XX		
XX	Sequence 181 AA:	

```

Query Match      Score 88; DB 14; Length 181;
Best Local Similarity 100.0%; Pctd. No. 1,5e+06;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;
          1 ILSKPEKFLQSSLALNRQM 19
          |||||
Cy         163 ILRSKEFLQSLLALRYQM 181
Db

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:35 (Search time 88.82 seconds
(without alignments)
16.295 Million cell updates/sec)

Title: us-09-202-104a-3

Sequence: 1 ILRSKREFQSSRLALRM 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the best score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	212	1 IVHNB2	interleukin-6 prec
2	59	67.0	212	1 I46621	interleukin-6 - pl
3	59	67.0	212	1 I46590	interleukin-6 - pl
4	58	65.9	208	2 T09216	interleukin-6 prec
5	52	59.1	208	1 A56610	interleukin-6 - sh
6	50	56.8	208	1 S29549	interleukin-6 prec
7	48	53.7	201	1 IC8K86	interleukin-6 prec
8	48	53.7	201	1 IC8K86	interleukin-6 prec
9	45	51.1	1082	2 H81582	hypothetical prote
10	44	50.0	207	2 I46084	interleukin 6 - ca
11	44	50.0	211	2 A34247	interleukin 6 - ca
12	44	50.0	610	2 T08597	dioI dehydratase-r
13	44	50.0	978	2 T40803	probable pre-tRNA
14	43.5	49.4	1159	2 T02866	hypothetical prote
15	43.5	49.4	1159	2 T02866	hypothetical prote
16	42	47.7	992	2 T46337	hypothetical prote
17	41	46.6	249	2 G64415	hypothetical prote
18	41	46.6	310	2 S35907	hypothetical prote
19	41	46.6	332	2 D83129	probable transcrip
20	41	46.6	427	2 T49122	hypothetical prote
21	41	46.6	461	2 JN0129	ID-myo-inositol-tr
22	41	46.6	461	2 JN0129	cardiomy-1 phosphat
23	41	46.6	517	2 B64372	hypothetical prote
24	41	46.6	596	2 T17333	coat protein gamma
25	41	46.6	831	2 T05265	coat protein gamma
26	41	46.6	2354	2 T13388	met-41 protein - f
27	40	45.5	251	2 H85781	hypothetical prote
28	40	45.5	271	2 B64532	hypothetical prote
29	40	45.5	315	2 T46156	hypothetical prote

30	40	45.5	532	2 B64123	CRP synthetase ctr
31	40	45.5	1017	2 PC4035	cell-cycle-depende
32	40	45.5	1024	2 F75489	cardiomy-1-phosphat
33	39	44.3	1024	2 F75489	cardiomy-1-phosphat
34	39	44.3	1024	2 F75489	cardiomy-1-phosphat
35	39	44.3	371	2 E83807	(5-methyl)lanthomet
36	39	44.3	398	2 A71482	hypothetical prote
37	39	44.3	437	2 J50237	hypothetical 48k p
38	39	44.3	454	2 C82682	glutamate-cysteine
39	39	44.3	484	2 XYR8C3	glycine hydroxymet
40	39	44.3	566	1 I64443	hypothetical prote
41	39	44.3	643	1 H85712	dark-type molecule
42	39	44.3	643	1 H85712	hypothetical prote
43	39	44.3	825	2 T23612	hypothetical prote
44	39	44.3	1051	2 T43355	cardiomy-1-phosphat
45	39	44.3	1161	2 A27069	lethal (2) giant 1

ALIGNMENTS

RESULT 1
1 IVHNB2
interleukin-6 precursor [validated] - human
N: Alternate names: B-cell differentiaton factor; B-cell hybridoma growth factor; B-c
on factor
C: Species: Homo sapiens (man)
C: Dates: 18-Dec-1987 sequence, revision 28-Dec-1997 *text change 08-Dec-2000
R: Yasukawa, K.; Hirano, T.; Matsuda, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A: Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) 9
A: Reference number: A32640; MUID:88082664
A: Accession: A32648
A: Molecule type: DNA
A: Residues: 1-212 <NID>
A: Cross-references: GB:004430; NID:q29494; PIDN:CA68278.1; PID:q29495
R: Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A: Title: Structure and expression of cDNA and genes for human interferon-beta-2, a dI
A: Reference number: A91051; MUID:87053818
A: Accession: A25692
A: Molecule type: mRNA
A: Residues: 1-212 <NID>
A: Cross-references: GB:004430; NID:q32673; PIDN:CA28026.1; PID:q32674
R: Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Matsuda, T.; Kishiyama
L. T.; Kishimoto, T.
Nature 324, 73-76, 1986
A: Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
A: Reference number: A93587; MUID:87065033
A: Accession: A33587
A: Molecule type: mRNA
A: Residues: 1-212 <NID>
A: Cross-references: GB:004602; NID:q33849; PIDN:CA28268.1; PID:q33850
R: Tomonuchi, N.; Miya, K.; Katsuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A: Title: Deletion of 3 untranslated region of human BSF-2 mRNA causes stabilization
A: Reference number: A33515; MUID:89351958
A: Accession: A33515
A: Molecule type: mRNA
A: Residues: 1-212 <NID>
A: Cross-references: GB:029150; NID:q186349; PIDN:AA59154.1; PID:q307063
R: Haegman, G.; Content, J.; Volckert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A: Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A: Accession: A25801; MUID:87004653
A: Molecule type: DNA; mRNA
A: Residues: 1-212 <NID>
A: Cross-references: GB:004403
A: Experimental source: Fibroblast
R: May, L.T.; Helgott, D.C.; Senegal, P.B.

[illegible]


```

Matches 13: Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALROM 19
||||:|||||:|||||
Db 194 ILRSLEDFQFSRLAIRIM 212

RESULT 3
146590
Interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1999 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: U01990
R:Metallman, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conce
A:Reference number: 146590; PMID:92360284
A:Accession: 146590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <SM>
A:Cross-references: GB:M80258; NID:q164514; PIDN:AAC27127.1; PID:q164515
C:Genetics:
A:Gene: IL-6
C:Superfamily: Interleukin-6

Query Match 67.0%; Score 59; DB 2; Length 212;
Best Local Similarity 66.4%; Pred. No. 0.023; 3; Mismatches 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALROM 19
||||:|||||:|||||
Db 194 ILRSLEDFQFSRLAIRIM 212

RESULT 4
709216
Interleukin 6 precursor - horse
C:Species: Equus caballus (domestic horse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C:Accession: T09216
R:Staden, R.; C.E.; Gorshov, D.R.
Nucleic Acids Res. 27, 146-150, 1999
A:Reference number: 216613
A:Accession: T09216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <SM>
A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388
C:Genetics:
A:Gene: IL-6
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor

Query Match 65.9%; Score 58; DB 2; Length 208;
Best Local Similarity 68.4%; Pred. No. 0.041; 3; Mismatches 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALROM 19
||||:|||||:|||||
Db 190 ILRSLEDFQFSRLAIRIM 208

RESULT 5
A56610
Interleukin-6 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A56610; S22162
R:Diogenes, L.; Cludis, I.; Kleuter, Y.; Kettmann, R.; Bury, A.
DNA Seq. 2, 411-413, 1992

```

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A:Title: Nucleotide sequence of bovine Interleukin-6 cDNA.
A:Reference number: A56610; PMID:93076003
A:Accession: A56610
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <SM>
A:Cross-references: EMBL:X57317; NID:q2193; PIDN:CAA0572.1; PID:g22594
A:Experimental source: BLV induced B cell lymphosarcoma
A>Note: sequence extracted from NCBI backbone (NCBI:P:118917)
C:Superfamily: Interleukin-6
C:Keywords: cytokine

Query Match 59.1%; Score 52; DB 1; Length 208;
Best Local Similarity 64.7%; Pred. No. 0.139; 3; Mismatches 3; Indels 0; Gaps 0;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALR 17
||||:|||||:|||||
Db 190 ILRSLEDFQFSRLAIR 206

RESULT 6
529549
Interleukin-6 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29549
R:Submitted to the EMBL Data Library, October 1992
A:Reference number: 529549
A:Accession: S29549
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <DB>
A:Cross-references: EMBL:X68723
C:Superfamily: Interleukin-6

Query Match 56.8%; Score 50; DB 1; Length 208;
Best Local Similarity 64.7%; Pred. No. 0.82; 2; Mismatches 4; Indels 0; Gaps 0;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRALR 17
||||:|||||:|||||
Db 190 ILRSLEDFQFSRLAIR 206

RESULT 7
ICM5
Interleukin 6 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
C:Accession: A30531; A27610; A30571; S01323; E34047; A26662; A40486; A60799;
R:Ranabe, O.; Akita, S.; Kamiya, T.; Wong, G.C.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A:Reference number: 327610; PMID:8816683
A:Title: The genomic structure of the murine IL-6 gene. High degree conservation of poten
A:Residues: 1-211 <SM>
A:Accession: A30531; A27610; PMID:8816683
A:Molecule type: DNA
A:Residues: 1-211 <SM>
A:Cross-references: GB:M20572; NID:q198369; PIDN:AA39302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Sakihara, J.P.; Renaldi, J.C.; Van Roost, E.; Boon, T.;
Bur, J.; Immunol. 16, 193-197, 1988
A:Reference number: 327610; PMID:8816683
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <SM>
A:Cross-references: GB:M06203; NID:g52701; PIDN:CA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.;

```

J. Immunol. 142, 1372-1376, 1989
 A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A:Accession: AF05711, MIMD:89124863
 A:Accession: AJ30571
 A:Molecule type: mRNA
 A:Residues: 5-211 <MOC>
 A:Cross-references: GB:MA4221; NID:9341131; PIDN:AA68814.1; PID:9870699
 R:Stimpson, R.J.; Moritz, R.L.; Rudlik, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino acid sequence and N-terminal sequence.
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166, 'X', 168-211 <SN>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R:Genet, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GBE>
 A:Cross-references: EMBL:X54542; NID:952727; PIDN:CAA38411.1; PID:952728
 R:Jahnen, M.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Stimpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Accession: B34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <AS>
 R:Van Snick, J.; Cayre, S.; Vink, A.; Dytche, C.; Coullie, P.G.; Rubira, M.R.; Stimpson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Accession: M2653
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A4486; MIMD:8901745
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHD>
 A:Cross-references: GB:J03783; NID:918367; PIDN:AAA9301.1; PID:9309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blankenstein, T.; Olin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a MC
 A:Reference number: S10241; MIMD:9017860
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:949738; PIDN:CAA3824.1; PID:9581860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Stimpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin
 A:Accession: S18254
 A:Molecule type: protein
 A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZMA>
 C:Genetics:
 A:Map position: 5
 A:Intras: 7/1, 68/3, 106/3, 156/3

C:Superfamily: Interleukin-6
 C:Cross-references: GB:MA4221; NID:9341131; PIDN:AA68814.1; PID:9870699
 R:Stimpson, R.J.; Moritz, R.L.; Rudlik, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino acid sequence and N-terminal sequence.
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166, 'X', 168-211 <SN>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R:Genet, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GBE>
 A:Cross-references: EMBL:X54542; NID:952727; PIDN:CAA38411.1; PID:952728
 R:Jahnen, M.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Stimpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Accession: B34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <AS>
 R:Van Snick, J.; Cayre, S.; Vink, A.; Dytche, C.; Coullie, P.G.; Rubira, M.R.; Stimpson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Accession: M2653
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A4486; MIMD:8901745
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHD>
 A:Cross-references: GB:J03783; NID:918367; PIDN:AAA9301.1; PID:9309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blankenstein, T.; Olin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a MC
 A:Reference number: S10241; MIMD:9017860
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:949738; PIDN:CAA3824.1; PID:9581860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Stimpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin
 A:Accession: S18254
 A:Molecule type: protein
 A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZMA>
 C:Genetics:
 A:Map position: 5
 A:Intras: 7/1, 68/3, 106/3, 156/3

C:Genetics:
 A:Map position: 5
 A:Intras: 7/1, 68/3, 106/3, 156/3

```

A:Gene: NMA0631
C:Superfamily: Neisseria meningitidis hypothetical protein NMA0631

Query Match          51.1% Score 45; DB 2; Length 1082;
Best Local Similarity 56.2%; P-Val 3D
Matches      9; Conservative    5; Mismatches     2; Indels   0; Gaps   0;

QY      4 SFKEFLOSSLRALRM 19
||:::||::|
Db       416 SFEKFOVSLKALRI 431

RESULT 10
Interleukin 6 - cat
C:Species: Felis silvestris catus (domestic cat)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I46084
C:Redundancy: M.O.: GDB99, C.: Kraus, L.; Good R.A.; Day, N.K.
P:Protein: Interleukin 6, p19
A>Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6
A:Reference number: I46084; MUID:94052249
A:Accession: I46084
A>Status: preliminary; translated from CB/BMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <RNA>
C:Cross-references: GB:I46914; NID:9438519; PIDN:AAA16620.1; PID:9438520
C:Superfamily: Interleukin-6

Query Match          50.0% Score 44; DB 2; Length 207;
Best Local Similarity 55.6%; Pred. No. 7.7;
Matches      10; Conservative    3; Mismatches     5; Indels   0; Gaps   0;

QY      2 IISKFELSSLRALRM 19
|||||
Db       190 LRLEDFQLRLAVRIM 207

RESULT 11
A:A34247
Interleukin-6 precursor - rat
Molecule type: mRNA
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northemann, W.; Bracchi, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A>Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells
A:Reference number: A34247; MUID:89380206
A:Accession: A34247
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NOR>
C:Cross-references: GB:M26744; NID:9204915; PIDN:AAA77659.1; PID:9204916
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match          50.0% Score 44; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 7.8;
Matches      8; Conservative    3; Mismatches     3; Indels   0; Gaps   0;

QY      1 IIRSFKEFLSSLRALRM 18
||:::||::|
Db       193 ILKALEDFLVKTRSTRO 210

RESULT 12
T08597
d:Species: Klebsiella oxytoca
d:Special: Klebsiella oxytoca

```

```
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C.Accession: T08597
R.Mori, K.; Tobimatsu, T.; Haru, T.; Toriya, T.
J. Biol. Chem. 272, 32034-32041, 1997
A.Title: Characterization, sequencing, and expression of the genes encoding a
A.Accession: J08597
A.Status: preliminary; translated from GB/EMBL/DDb
A.Molecule type: DNA
A.Residues: 1-610 <MOR>
A.Cross-references: EMBL:AF017781; NID:g3115375; PTDN:MCI5871.1; PID:g3115376
C.Genetics:
C.Description:
C.Function:
A.Description: probably a reactivating factor for inactivated diol dehydratase
A.Note: large chain
C.Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain

Query Match          50.0%; Score 44; DB 2; Length 610;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 12; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Oy      1 IIRSFRE--FLOSSIALROM 19
        |||||
Db       520 IIRSAKEVFYFNALRALIKOV 540

RESULT 13
T08083
Probable pre-tRNA nuclear export receptor - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
R.Check A.: Reinhardt, R.; Tyne, M.; Rajandream, M.A.; Barrell, B.G.
A.Accession: T08083
A.Reference number: Z21949
A.Cross-references: EMBL:D81482; DDB Library, October 1998
A.Molecule type: DNA
A>Status: preliminary; translated from GB/EMBL/DDb
A.Residues: 1-978 <REC>
A.Cross-references: EMBL:A0132684; PTDN:CA21794.1; SPDB:SFB6887_09c
A.Experimental source: strain 97Zh-; Clone PI p887
A.Cone: SPOB.SPBP87_09c
A.Map position: 2

Query Match          50.0%; Score 44; DB 2; Length 978;
Best Local Similarity 53.3%; Pred. No. 39;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy      3 RSERETGSSRARLR 17
        |||||
Db       960 RSFPQPFQRKQLK 974

RESULT 14
T02866
Typochelatal protein CAC2 [imported] - Leishmania major (strain Friedlin)
C.Species: Leishmania major
C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C.Accession: F81464; T02866
R.Rhyler, P.J.; Audleman, L.; DeVos, T.; Hixon, G.; Klaser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A>Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A.Reference number: AB1455; WUID:9917897
A.Accession: F81464
A.Status: preliminary; translated from GB/EMBL/DDb
A.Molecule type: DNA
A.Cross-references: EMBL:AB001274; NID:g364850; PTDN:MCC24689.1; PID:g3006218; SPDB:Q
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GenCode version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:13 : Search time 48.45 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-09-202-104A-3

Protein score: 81

Sequence: 1 IIRSFKEFIQSSIRALRQW 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	ID	Description
1	88	100.0	212	1 IL6_CERRO	P46590 cerrobobus
2	88	100.0	212	1 IL6_HUMAN	P05231 homo sapien
3	88	100.0	212	1 IL6_MACCA	P73341 macaca fasc
4	85	96.6	212	1 IL6_MACMU	P41494 mus musc
5	85	97.0	212	1 IL6_MOUSE	P41493 mus musc
6	85	97.0	212	1 IL6_MOUSE	P41493 mus musc
7	58	65.9	207	1 IL6_CANRA	P41332 sus scrofa
8	58	65.9	207	1 IL6_HORSE	P05181 equus caball
9	58	65.9	209	1 IL6_PROVT	Q28813 phoca vitul
10	55	62.5	205	1 IL6_ORCOR	Q28747 orctinus orc
11	55	62.5	208	1 IL6_CAPII	Q28319 capra hircu
12	55	62.5	208	1 IL6_SHEPP	P23455 ovis aries
13	55	62.5	208	1 IL6_SHEPP	P23455 ovis aries
14	52	59.1	209	1 IL6_BOVIN	P23455 ovis aries
15	49	55.7	208	1 IL6_PICHA	P41681 felis silve
16	48	54.5	211	1 IL6_MOUSE	P05605 mus muscul
17	48	54.5	201	1 MGF_CHICK	P13854 gallus galli
18	44	50.0	211	1 IL6_RAT	P02607 rattus norv
19	41	46.6	249	1 Y927_METUA	Q05137 mycoplasma
20	41	46.6	310	1 ADPR_LACLA	Q06713 lactococcu
21	40	45.5	271	1 Y927_METUA	Q05137 mycoplasma
22	40	45.5	310	1 Y927_METUA	Q05137 mycoplasma
23	40	45.5	310	1 Y927_METUA	Q05137 mycoplasma
24	39	44.3	371	1 TRMU_HUMAN	P43454 homo sapien
25	39	44.3	483	1 GLYC_RAITY	P07511 oryctolagus
26	39	44.3	566	1 Y397_MYCCE	P47637 mycoplasma
27	39	44.3	635	1 HS68_DROME	Q09122 drosophila
28	39	44.3	636	1 HS68_DROME	Q09122 drosophila
29	39	44.3	636	1 HS68_DROME	Q09122 drosophila
30	39	44.3	640	1 HS72_ANOAL	P41825 anopheles a
31	39	44.3	641	1 HS72_DROME	P02824 drosophila
32	39	44.3	642	1 HS70_DROME	P82910 drosophila
33	39	44.3	643	1 HS71_DROME	P02825 drosophila

34	39	44.3	649	1 HS70_CHIRE	P25840 chlamydomon
35	39	44.3	1051	1 CARB_SUILO	Q05969 sulfolobus
36	39	44.3	1161	1 L26L_DROME	P08411 drosophila
37	39	44.3	1166	1 L26L_DROME	P08411 drosophila
38	39	44.3	1166	1 L26L_DROME	P08411 drosophila
39	38	43.2	314	1 IL15_MOUSE	P48346 mus muscul
40	38	43.2	329	1 IPNS_STRJU	P18266 streptococ
41	38	43.2	347	1 YF66_MYCPN	P75194 mycoplasma
42	38	43.2	558	1 YF66_MYCPN	P75194 mycoplasma
43	38	43.2	1967	1 YG50_YEAST	Q00597 homo sapien
44	38	43.2	3038	1 TRIO_HUMAN	P53327 saccharomyc
45	37	42.0	119	1 R8E8_SUILO	P95930 sulfolobus

ALIGNMENTS

RESULT 1

ID IL6_CERRO STANDARD: PRT: 212 AA.

AC P46590

DT 01-NOV-1995 (Rel. 32, Created)

DE 15-JUL-1998 (Rel. 36, Last sequence update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

IL6.

Cercobobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Placentalia; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Cercobobus.

OX NCBI_TaxID=9531;

[1]

SEQUENCE FROM N. A.

STRAIN=FLU.

MDLID=96003435; PubMed-7561102;

RA Villinger F.J., Brar S.S., Wayne A.E., Chikala N., Ansari A.A.;

RT Comparative sequence analysis of cytokine genes from human and

FI dominant primate species (1995).

CC - FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HERPETOCTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

CC - SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: I26013; AA959972.1; -

DR HSFP: P05231; IAUU.

DR InterPro: IP8003573; IL6_MGF_GCSF.

DR InterPro: IP8003574; Interleukin-6.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFMGF.

DR PRINTS: PR00433; INTERLEUKIN-6.

DR SMART: SM00126; IL6; IL6ILKIN-6; 1.

DR PROSITE: PS00254; INTERLEUKIN-6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29

FT CHAIN 30 212

FT DISULFID 72 118

FT DISULFID 171 173

FT CARBOHYD 172 172

FT CARBOHYD 212 AA: 23668 MW: C73C0352684B95 CRC64;

Query Match 100.0% Score 88. DB 1. Length 212.
 E-value Similarity 100.0% E-value 2.5e-07.
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 IIRSFEPLOSIRALNOM 19
 DB 194 IIRSFEPLOSIRALNOM 212
 IIRSFEPLOSIRALNOM 19
 IIRSFEPLOSIRALNOM 212
 RESULT 2
 IL6_HUMAN STANDARD PART: 212 AA.
 AC P05231;
 DT 13-AUG-1987 (rel. 05, Last sequence update)
 DT 13-AUG-1987 (rel. 05, Last annotation update)
 DE INTERLEUKIN-6 (IL-6) (BETA-2-MACROGLOBULIN-INDUCIBLE GENE)
 DE INTERFERON BETA-2 (HYBRIDOMA GROWTH FACTOR 2) (BSF-2)
 DE IL6 OR IFNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RA MEDLINE-87065033; PubMed-3491322.
 RA Hirano T., Yasukawa K., Harada H., Taga T., Matsumoto Y., Matsuda T.,
 Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tanasawa S.,
 Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 B. Complementary DNA for a novel human interleukin (BSF-2) that induces
 B lymphocytes to produce immunoglobulin.*
 RT J. Biol. Chem. 264:15780(1989).
 RM [12]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-8808264; PubMed-3500852.
 RA Yasukawa K., Hirano T., Matsumoto Y., Muratani K., Matsuda T.,
 Naito S., Kishimoto T.;
 RA Structure and expression of human B cell stimulatory factor-2
 (BSF-2).
 RT J. Biol. Chem. 264:2945(1989).
 RM [13]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-87067433; PubMed-3538015.
 RA May L.T., Heligott D.C., Sehgal P.B.;
 RA Anti-beta-2-interferon antibodies inhibit the increased expression of
 IL-6 mRNA in tumor necrosis factor- α -induced human fibroblasts.
 RT J. Biol. Chem. 264:5415(1989).
 RM [14]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-87053818; PubMed-3023045.
 RA Zilberstein A., Ruggieri R., Koro J.H., Revel M.;
 RA Structure and expression of cDNA and genes for human
 interferon-beta-2, a distinct species inducible by growth-stimulatory
 factor.
 RT J. Biol. Chem. 264:2537(1989).
 RM [15]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-8808786; PubMed-3320204.
 RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 Aarden L.A.;
 RA Molecular cloning and expression of hybridoma growth factor 1a
 (BSF-2).
 RT J. Immunol. 139:4116(1987).
 RM [16]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89391958; PubMed-2789513.
 RA Tomouchi N., Miwa K., Kariyayama H., Matsui H.;
 RA Deletion of 3' untranslated region of human BSF-2 mRNA causes
 stabilization of the mRNA and high-level expression in mouse NIH3T3
 cells.*
 RT J. Biol. Chem. 264:1056(1989).
 RM [17]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-87004683; PubMed-3758081.
 RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 Fiers W.;
 RA Structural analysis of the sequence coding for an inducible 26-kDa
 protein in human fibroblasts.*
 RT Eur. J. Biochem. 159:625(1986).
 RM [18]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89193117; PubMed-3266463.
 RA Wong G., Mitei-Gianotti J., Hewick R., Clark S., Ogawa M.;
 RA Interleukin 6: Identification as a hematopoietic colony-stimulating
 factor.*
 RT Behring Inst. Mitt. 83:40(1988).
 RM [19]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93178270; PubMed-1291250.
 RA Chen O. Y.;
 RA Stable and efficient expression of human interleukin-6 cDNA in
 mammalian cells after gene transfer.*
 RT Chung-Hua Chung Lin Tsa Chih 14:340-344(1992).
 RM [20]
 RP SEQUENCE OF 30-53.
 RA MEDLINE-89154445; PubMed-3279111f.
 RA van Damme J., van Beuven J., Decock B., van Snick J., de Ley M.,
 Billiau A.;
 RA Separation and comparison of two monokines with
 lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 factor (HGF). Identification of leukocyte-derived HGF as IL-6.*
 RT J. Immunol. 140:1534-1541(1988).
 RM [21]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 157 DISULFIDE BOND.
 RA MEDLINE-9514344; PubMed-785144f.
 RA Breton J., la Plante A., Bertolero F., Orsini G., Valsesia B.,
 Zilio R., de Philippis V., Polverio de Laureto P., Fontana A.;
 RA Structure, stability and biological properties of a N-terminally
 truncated form of recombinant human interleukin-6 containing a single
 disulfide bond.*
 RT J. Biol. Chem. 264:573-581(1989).
 RM [22]
 RP DISULFIDE BONDS.
 RA MEDLINE-89286115; PubMed-2472117.
 RA Clogston C.L., Boone T.C., Cranelli B.C., Mendiaz E.A., Lu H.S.;
 RA Disulfide structures of human interleukin-6 are similar to those of
 human granulocyte colony-stimulating factor.*
 RT J. Biol. Chem. 264:1144-1151(1989).
 RM [23]
 RP MUTAGENESIS.
 RA MEDLINE-91243808; PubMed-2037043.
 RA Luetjens C., Kruetgen A., Koeber G., Heintz P.C., Rose-John S.;
 RA Evidence for the importance of a positive charge and an
 alpha-helical structure of the C-terminus for biological activity of
 human IL-6.*
 RT J. Biol. Chem. 264:265-267(1989).
 RM [24]
 RP STRUCTURE BY NMR.
 RA MEDLINE-96134845; PubMed-8555185.
 RA Nishimura C., Matsumoto H., Gouda H., Shimada I., Arata Y.;
 RA Polymorphic topologies of human interleukin-6 and its mutants as studied
 by NMR spectroscopy.*
 RT Biochemistry 35:273-281(1996).
 RM [25]
 RP STRUCTURE BY NMR.
 RA MEDLINE-97303053; PubMed-9159484.
 RA Xu G.-Y., Yu H.-A., Hong J., Stehl M., McDonough T., Kay L.E.,
 Sumlin D.A.;
 RA Solution structure of recombinant human interleukin-6.*
 RT J. Mol. Biol. 268:468-481(1997).
 RM [26]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE-97224126; PubMed-9118960.


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RX MEDLINE-96003435; PubMed-7561102;
RA Villinger P.J., Bear S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT nonhuman primates: the analysis of cytokine genes from human and
CC PubMed-1553946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPAOCYTES IT INDUCES ACUTE PHASE REACTANTS (BT SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@1sb-sdb.ch).
CC -----
CC EMBL: L26028; AAA9978.1; -.
CC HSP: P05231; IALU.
CC InterPro: IPRO03573; IL6_MGF_GCSF.
CC InterPro: IPRO03574; Interleukin-6.
CC Pfam: PF00489; IL6.
CC Pfam: PF00489; IL6.
CC PRINTS: PR00434; INTERLEUKIN6.
CC PRODOM: PD004356; Interleukin_6; 1.
CC SMART: SM00126; IL6; 1.
CC PROSITE: PS00254; INTERLEUKIN_6; 1.
CC CYCLOPE: Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC FT DISULFID 70 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 N-LINKED (GLUCNA... ) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLUCNA... ) (POTENTIAL).
CC SEQUENCE 212 AA; 23728 MW; 4130DFECF08C6D CMC64;
CC -----
Query Match 66.44; Score 85; DB 1; Length 212;
Best Local Similarity 90.74; Pval: 8.8e-07; Mismatches 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 0; Indels 0;
CC 1 ILIRSEFELGSSIRALROM 19
CC 194 ILIRSEFELGSSIRALROM 212
CC -----
RESULT 5
ID IL6_MUSVI STANDARD: PRT: 125 AA.
AC P41693;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
CC INTERLEUKIN-6 (IL-6) (PROMOTER).
CC MUSTELA vison (American mink).
CC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
CC NCBI_TaxID=9667;
CC [1]
CC SEQUENCE FROM N.A. Parayan S.M., Wolfsharper J.B.;
CC Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPAOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----

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CC or send an email to license@1sb-sdb.ch).
CC -----
CC EMBL: U34105; AAA6829.1; -.
CC HSP: P05231; IALU.
CC InterPro: IPRO03573; IL6_MGF_GCSF.
CC Pfam: PF00489; IL6; 1.
CC SMART: SM00126; IL6; 1.
CC PROSITE: PS00254; INTERLEUKIN_6; 1.
CC CYCLOPE: Glycoprotein; Growth factor.
CC NON_TER 1 26 BY SIMILARITY.
CC FT DISULFID 16 34 POTENTIAL.
CC SEQUENCE 125 AA; 14604 MW; 9262DD3BA98966A CMC64;
CC -----
Query Match 67.04; Score 59; DB 1; Length 125;
Best Local Similarity 68.44; Pval: No. 0.0078;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC 1 ILIRSEFELGSSIRALROM 19
CC 107 ILIRSEFELGSSIRALROM 125
CC -----
RESULT 6
ID IL6_PIG STANDARD: PRT: 212 AA.
AC P41693;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC INTERLEUKIN-6 (IL-6).
CC Sus scrofa (Pig).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
CC NCBI_TaxID=9623;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE-91338547; PubMed-1873476;
CC Richards C., Saklatvala J.;
CC "Molecular cloning and sequence of porcine interleukin 6 cDNA and
CC expression of cDNA in synovial fibroblasts in vitro.";
CC J. Interleukin 31:65-70(1991).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE-92360284; PubMed-1497880;
CC Machalalan N., Bixby J.A., Roberts M.R.;
CC "Expression of interleukin-6 in porcine, ovine, and bovine
CC preimplantation conceptuses.";
CC J. Reprod. Dev. 32:324-330(1992).
CC [3]
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPAOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL: M6072; AAC7133.1; -.
CC HSP: P05231; IALU.
CC NCBI_TaxID=9623;

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FT	CHAIN		28	208	INTERLEUKIN-6.
FT	DISULFID		69	75	BY SIMILARITY.
FT	CYSRSD		98	108	BY SIMILARITY.
FT	CHNRD		72		N-LINKED (GLCNAC...) (POTENTIAL).
FT	CONFLICT		14	18	I -> I (IN REF. 1).
FT	CONFLICT		8	8	I -> I (IN REF. 3).
FT	CONFLICT		137	137	I -> V (IN REF. 2).
FT	CONFLICT		205	205	V -> I (IN REF. 3).
SO	SEQUENCE		208 AA:	23325 MW;	A62FAFC23405BFE66 CRC64;

Query Match		55.9%	Score 58.	DP 1:
Best Local Similarity		66.4%	PctId No.	0.02
Matches	13:	Conservative	3:	Mismatches
			3:	Indels
			0:	Gaps
			0:	


```

OY      1 ILNSKFETLOSSLALAFROM 19
        |||||:::|||::|||::|
Db       190 ILRSLLDFPLDFSLAVALRM 208

RESULT  9
ID       IL6_PROV1          STANDARD:    PRT:   209 AA.
AC       Q28B19;
DT       30-MAY-2000 (Rel. 39, Created)
DT       30-MAY-2000 (Rel. 39, Last sequence update)
DT       30-MAY-2000 (Rel. 39, Last annotation update)
GI       INTERLEUKIN-6 PRECURSOR (IL-6) (PROKARYOT).
GN       IL6
RL       Phoca vitulina (Harbor seal).
OS       Phoca vitulina (Harbor seal).
OC       Eukaryota; Metazoa; Chordata; Cetartata; Vertebrata; Euteleostomi;
NC       Mammalia; Eutheria; Carnivora; Plomipedia; Procidae; Phoca.
OX       NCBI_TaxID=9720;
RN       11
RP       SOURCE FROM N.A. PubMed=6837817;
RA       Kung D.P., Scherrell M.D., McKnight M.L., Redalson T.H., Hann R.D.,
RA       Scott J.L., Ferrick D.A.; McKnight M.L., Redalson T.H., Hann R.D.,
RA       "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RA       the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and from
RA       Southern sea otter (Enhydra lutris nereis).";
RA       Immunogenetics 43:190-193(1996).
RL       FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
RL       FUNCTIONS. IT PROMOTES PROLIFERATION AND DIFFERENTIATION
RL       OF B CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
RL       PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
RL       HEPATOCYTES IT INDICATES ACTIVE PHASE REAGENTS (BY SIMILARITY).
CC       -1- SUBCELLULAR LOCATION: SECRETED.
CC       -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC       THIS SEQUENCE BELONGS TO THE IL-6 SUPERFAMILY.
CC       BETWEEN THE Swiss Institute of Bioinformatics and the European Bioinformatics Institute, there are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
CC       entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC       PMID: 146802; .AA01430.1.
CC       EMBL: L46802; .AA01430.1.
DR       Cytokine; Glycoprotein; Growth factor; Signal.
DR       CHOKLINE;
DR       STIMAN;
DR       CHAIN;
DR       DISULFID;
DR       DISULFID;
DR       SEQUENCE
        209 AA: 23483 MW; 75144922AC43BA8B9 CRC64;

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01      65.9%: Score 58; db 1; Length 205;
02      Best Local Similarity 68.4%; Pred. No. 0.02;
03      Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
04
05      1 ILNSREF:QSSIALRQM 19
06      1111 : 1111 : 1111
07      191 ILNSLDD:QSSIALRQM 209
08
09      RESULT 10
10      IL6.ORCOR
11      ID IL6.ORCOR STANDARD: PRT. 205 AA.
12
13      AC 028747;
14      30-MAY-2000 (Rel. 39; Created)
15      30-MAY-2000 (Rel. 39; Last sequence update)
16      30-MAY-2000 (Rel. 39; Last annotation update)
17      30-MAY-2000 (Rel. 39; Last modification)
18      116
19      IL6
20      Orcinus orca (Killer whale).
21      Eukaryota; Metazoa; Chordata; Ctenista; Vertebrata; Euteleostomi;
22      Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
23      Orcinus.
24      NCBI_TaxID=9733;
25      (1)
26      SEQUENCE FROM N.A.
27      MEDLINE=96163018; PubMed=9575817;
28      MESH=96163018; EMBL=9575817;
29      Scott J., Perlick D.A., McWhight M.L., Rolderson T.H., Hanni K.D.,
30      "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
31      the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
32      Southern sea otter (Enhydra lutris nereis).";
33      Immunogenetics 43:190-195(1996).
34      - FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
35      FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
36      OF B-CELLS INTO ANTI-SECRETING CELLS. IL6 INDUCES PROLIFERATION
37      OF T-CELLS AND INDUCES THE RELEASE OF INTERFERON-GAMMA. IL6 IS AN
38      HEPATOCYTE-INDUCIBLE KINASE RECEPTOR. IL6 IS A MEMBER OF THE
39      IL-6 SUPERFAMILY.
40      - SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
41
42      CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
43      between the Swiss Institute of Bioinformatics and the EMBL outstation at
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47      or send an email to license@isb.scrib.ch)
48
49      CC EMBL; LA6803; AAB01429.1; -.
50      DR HSSP; P05231; IAU;
51      DR InterPro; IPR003573; IL6_MSF_GCSF;
52      DR InterPro; IPR003574; Interleukin_6;
53      Pfam; PF00489; IL6; 1.
54      SMART; SM00126; IL6; Interleukin_6; 1.
55      DR Cytokine; Glycoprotein; Growth factor; Signal.
56      PT NON TER 1
57      FT SIGNAL <1 21 BY SIMILARITY.
58      FT CHAIN 22 205 INTERLEUKIN-6.
59      FT DISULFID 64 70 BY SIMILARITY.
60      FT DISULFID 93 103 BY SIMILARITY.
61      CARBOHYD 164 164 N-LINKED (GLCNAC... ) (POTENTIAL).
62      SSOURCE 205 AA; 2326 MW; 6308F3M457960832 CR64;
63
64      Query Match 62.5%; Score 55; db 1; Length 205;
65      Best Local Similarity 70.5%; Pred. No. 0.059;
66      Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
67
68      1 ILNSKFLOSSIALMR 17
69      1111 : 1111 : 1111

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AC P26892; 01-AUG-1992 (rel. 23, Created)
 DT 01-AUG-1992 (rel. 23, last sequence update)
 DT 01-JUL-1998 (rel. 23, last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bovinae; Bos.
 CC [1] taxid=9913.
 RN [1] taxid=9913.
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN.
 RA MEDLINE=93076003; PubMed=1446077;
 RA Drogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
 RA Nucleotide sequence of bovine interleukin-6 cDNA.
 CC FUNCTION: IL-6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC or send an email to license@sdb-sdb.ch).
 DR EMBL: X57317; CAA60572.1; -
 DR PIR: S22162; S22162.
 DR HSSP: P05231; 2116.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin-6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMP.
 DR PROSITE: PS00436; INTERLEUKIN6.
 DR Prodom: PD00436; Interleukin-6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYCLINE: Glycoprotein; Growth factor; Signal.
 RN SIGNAL: 1
 RN CHAIN: 29
 RN DISULFID: 70
 RN DISULFID: 70
 FT DISULFID 101 111
 FT CARBOHYD 38 38
 SEQUENCE 208 AA; 23758 MW; A0F009B9A2EC341 CRC64;
 Query Match 59.1%; Score 52; DB 1; Length 208;
 Best Local Similarity 62.7%; PctIdent 0.16;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 ILRSKFPGSSRLAR 17
 DB 190 ILRNLEPFGTFLRAIR 206
 RESULT 14
 ID IL6_MOUSE STANDARD; PRT: 207 AA.
 AC 035736;
 DT 15-JUL-1999 (rel. 38, Created)
 DT 15-JUL-1999 (rel. 38, last sequence update)
 DT 15-JUL-1999 (rel. 38, last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Mus musculus (Woodchuck).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Scuriromachi; Scuridae; Scurinae;
 CC Murinae.
 CC [1] taxid=9995.
 RN [1] taxid=9995.
 RP SEQUENCE FROM N.A.
 RC TISSUE-Peripheral blood;
 RA MEDLINE=98139533; PubMed=9472070;
 RA Lothangel B., Lu M., Rogendorf M.;
 RA Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
 CC and interleukin 47-332-335(1998).
 CC FUNCTION: IL-6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 DR EMBL: Y14139; CAA74571.1; -
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin-6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMP.
 DR PROSITE: PS00436; INTERLEUKIN6.
 DR Prodom: PD00436; Interleukin-6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYCLINE: Glycoprotein; Growth factor; Signal.
 RN SIGNAL: 1
 RN CHAIN: 18
 RN DISULFID 19 207
 RN DISULFID 95 104
 FT DISULFID 95 104
 FT CARBOHYD 101 101
 SEQUENCE 207 AA; 23770 MW; F3D019F66D6A600 CRC64;
 Query Match 58.0%; Score 51; DB 1; Length 207;
 Best Local Similarity 55.6%; PctIdent 0.26;
 Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ILRSKFPGSSRLAR 18
 DB 189 ILRNLEPFGTFLRAIR 206
 RESULT 15
 ID IL6_HUMAN STANDARD; PRT: 208 AA.
 AC P41683;
 DT 01-NOV-1995 (rel. 32, Created)
 DT 01-NOV-1995 (rel. 32, last sequence update)
 DT 15-JUL-1998 (rel. 36, last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Heliobacterium catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedes; Felidae; Felis.
 CC NCBI_TaxID=9685.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94162386; PubMed=8117820;
 RA Ohashi T., Matsumoto Y., Watarai T., Gotsuka R., Tsujimoto H.,
 RA Nagasawa A.;
 RA Molecular cloning of feline interleukin-6 cDNA.
 DT J Vetr. Med. Sci. 55:941-944(1993).
 RN [2]

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:19 ; Search time 157.32 Seconds
(without alignments)
17.656 Million cell updates/sec

File: us-09-202-104a-3

Matrix score: 1 ILRSKFLOSLSRALQM 19

Sequence: 1 ILRSKFLOSLSRALQM 19

Scoring table: GAPCP 10.0 , Gapext 0.5

Searched: 473505 seqs, 146273329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPRENBL17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mollusc:*
8: sp.oranellie:*
9: sp.phage:*
10: sp.plant:*
11: sp.rentent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	73	83.0	209	6	097540	097540 actus nancy
2	73	83.0	209	6	097TH3	097TH3 actus lemut
3	58	65.9	207	6	09WV27	09WV27 actus lemut
4	54	61.4	207	6	028403	028403 embrya lut
5	54	61.4	207	11	09JH03	09JH03 delphina lut
6	51	54.0	207	11	09JH03	09JH03 delphina lut
7	49	55.7	94	6	062775	062775 felis silve
8	47	53.4	118	6	09W420	09W420 sylviagus
9	47	53.4	118	6	09W420	09W420 sylviagus
10	47	53.4	118	6	09W420	09W420 sylviagus
11	45	53.4	118	6	09W420	09W420 sylviagus
12	45	53.4	118	6	09W420	09W420 sylviagus
13	45	53.4	118	6	09W420	09W420 sylviagus
14	45	53.4	118	6	09W420	09W420 sylviagus
15	45	53.4	118	6	09W420	09W420 sylviagus
16	45	53.4	118	6	09W420	09W420 sylviagus
17	44	50.0	108	6	09BD15	09BD15 phococoid
18	44	50.0	108	6	09BD15	09BD15 phococoid
19	44	50.0	108	6	09BD15	09BD15 phococoid
20	44	50.0	108	6	09BD15	09BD15 phococoid

20	44	50.0	772	3	09HGHO	09HGHO clavispora
21	44	50.0	978	3	094258	094258 schizosach
22	43.5	49.4	1159	5	060981	060981 leishmania
23	42	47.7	236	5	09VLM0	09VLM0 dirosophila
24	42	47.7	236	5	09VLM0	09VLM0 dirosophila
25	42	47.7	236	5	09VLM0	09VLM0 dirosophila
26	42	47.7	236	5	09VLM0	09VLM0 dirosophila
27	42	47.7	236	5	09VLM0	09VLM0 dirosophila
28	42	47.7	236	5	09VLM0	09VLM0 dirosophila
29	42	47.7	236	5	09VLM0	09VLM0 dirosophila
30	42	47.7	236	5	09VLM0	09VLM0 dirosophila
31	41	46.6	332	2	0912X0	0912X0 pseudomonas
32	41	46.6	332	2	0912X0	0912X0 pseudomonas
33	41	46.6	332	2	0912X0	0912X0 pseudomonas
34	41	46.6	332	2	0912X0	0912X0 pseudomonas
35	41	46.6	332	2	0912X0	0912X0 pseudomonas
36	41	46.6	332	2	0912X0	0912X0 pseudomonas
37	41	46.6	332	2	0912X0	0912X0 pseudomonas
38	41	46.6	332	2	0912X0	0912X0 pseudomonas
39	41	46.6	332	2	0912X0	0912X0 pseudomonas
40	41	46.6	332	2	0912X0	0912X0 pseudomonas
41	41	46.6	332	2	0912X0	0912X0 pseudomonas
42	40	45.5	126	5	09W420	09W420 sylviagus
43	40	45.5	126	5	09W420	09W420 sylviagus
44	40	45.5	126	5	09W420	09W420 sylviagus
45	40	45.5	126	5	09W420	09W420 sylviagus

ALIGNMENTS

RESULT 1

ID 097540 PRELIMINARY; PRT, 209 AA.

DT 01-MAY-1999 (TREMBLrel, 10, Created)

DT 01-MAY-1999 (TREMBLrel, 11, Last sequence update)

DT 01-JUN-2001 (TREMBLrel, 12, Last annotation update)

DE INTERLEUKIN-6 (FRAGMENT)

GN IL-6

OS Actus nancyanae (owl monkey)

OC Eukaryota; Metazoa; Chordata; Granulata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Actus;

OX NCBI:Taxid=97293;

RA SOURCE FROM N.A.

RA Behavory S.J., Hernandez E., Moreno A., Patariroyo M.E., Murillo L.A.;

RT Identification, cloning and sequencing of different interleukin genes

RT In 4 Actus species.

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: A014510; A001536.1; -

DR HSP: F053333; H003573; IL6_MGF_GCSF.

DR HSP: F053333; H003573; IL6_MGF_GCSF.

DR HSP: F053333; H003573; IL6_MGF_GCSF.

DR HSP: F053333; H003573; IL6_MGF_GCSF.

DR HSP: F053333; H003573; IL6_MGF_GCSF.

ID 09PMH3 PRELIMINARY: PRT: 209 AA.
 AC 09PMH3: 09PMH3.2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus lemurinus (Northern gray-necked night monkey), Euteleostomi;
 OC Euharyota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 NC NCM1_TaxID=43147;
 RX NCM1_TaxID=43147;
 RA SEQUENCE FROM N.A.
 RA Murillo L.A., Hernandez E., Echaverry S.J., Mendez J.A.,
 RA Patarroyo M.E.;
 RL Aotus lemurinus gene for IL-6.*
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL Accession: U09192; Length: 1256; 1.
 RA HSP: P03231; ILM: 1.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 FT NON_TER
 FT PROSITE: PS00254; INTERLEUKIN_6; 1.
 SEQUENCE 209 AA; 23115 MW; A0ADPMAAF56GCC CRC64;

Query Match 83.0%; Score 73; DB 6; Length 209;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IIRSFREFLOSSIRALM 16
 Db 194 IIRSFREFLOSSIRAL 209

RESULT 3
 09MTZ7 PRELIMINARY: PRT: 207 AA.
 AC 09MTZ7:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Canis familiaris (dog).
 OC Euharyota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 NC NCM1_TaxID=9615;
 RX NCM1_TaxID=9615;
 RA SEQUENCE FROM N.A.
 RA Youn H.-Y., Shio I.-S.;
 RL Canine IL-6 mRNA.*
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL Accession: U09192; Length: 1665; 1.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 SEQUENCE 207 AA; 23042 MW; 4551AE01C80F50 CRC64;

Query Match 65.9%; Score 58; DB 6; Length 207;
 Best Local Similarity 68.4%; Pred. No. 0.013;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IIRSFREFLOSSIRALM 19
 Db 189 IIRSFREFLOSSIRALM 207

RESULT 4
 ID 028403 PRELIMINARY: PRT: 207 AA.
 AC 028403:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Euharyota luris (Sea otter).
 OC Euharyota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 NC NCM1_TaxID=34882;
 RX NCM1_TaxID=34882;
 RA SEQUENCE FROM N.A.
 RA Scott J.P., Schreiner M.D., McNight M.L., Reidson T.H., Hanni K.D.,
 RA Kind D.P., Schreiner M.D., McNight M.L., Reidson T.H., Hanni K.D.,
 RA Scott J.P., Ferrick D.A.;
 RL *Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RL the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RL immunogenetics 43:190-195(1996).
 RL EMBL: L4804; Accession: 1996.
 RL Accession: U09192; Length: 1256; 1.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 FT NON_TER
 FT PROSITE: PS00254; INTERLEUKIN_6; 1.
 SEQUENCE 207 AA; 23527 MW; 729ECCD9113608B CRC64;

Query Match 61.4%; Score 54; DB 6; Length 207;
 Best Local Similarity 63.2%; Pred. No. 0.58;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IIRSFREFLOSSIRALM 19
 Db 189 IIRSFREFLOSSIRALM 207

RESULT 5
 09XT80 PRELIMINARY: PRT: 208 AA.
 AC 09XT80:
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE INTERLEUKIN 6 PRECURSOR.
 OS Delphinapterus leucas (beluga whale).
 OC Euharyota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 NC NCM1_TaxID=9745;
 RX NCM1_TaxID=9745;
 RA SEQUENCE FROM N.A.
 RA St-Laurent G., de Guise S., Fournier M., Archambault D.;
 RL *Molecular cloning and phylogenetic analysis of beluga whale
 RL (Delphinapterus leucas) interleukin 6.*
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF076643; Accession: 1998.
 RL Accession: U09192; Length: 1665; 1.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 SEQUENCE 208 AA; 23456 MW; 61CC8CCE8039C4 CRC64;

Query Match 61.4%; Score 54; DB 6; Length 208;

[illegible]

```

RL Cytokine.12:555-565(2000).
DR EMBL: AF161818; AAF6564.1.
RC TISSUE=OVARY.
DR PIR: P00489.1; IL6_MGF_GCSF.
DR PRINTS: PR00433; IL6CSFPGF.
DR SMART: SM00126; IL6: 1.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN.1.
FT NON_TER
SQ SEQUENCE 118 AA: 1834 MW: 62937BD3BDDAABC CRC64:
SO

Query Match 53.4%: Score 47; DB 6; Length 118;
Best Local Similarity 52.6%: Pred. No. 4.3;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSFKEFLQSSIRALROM 19
DB 100 ILRLMDTDFQSLRAVGM 118
|||||:|||||:|

RESULT 10
O9MZ08 PRELIMINARY: PRT; 118 AA.
AC O9MZ08: 01-OCT-2000 (TRIMBLREL. 15; Created)
DT 01-OCT-2000 (TRIMBLREL. 15; Last sequence update)
DR 01-JUN-2001 (TRIMBLREL. 17; Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
IL-6.
CN Lepus californicus (Black-tailed jackrabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
CX NCBI_TaxID=48087;
DR TISSUE=OVARY.
RC MEDLINE-20304414; PubMed-10943729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
*The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
European rabbit (Oryctolagus cuniculus).";
DR EMBL: AF161818; AAF6564.1.
DR PIR: P00489.1; IL6_MGF_GCSF.
DR PRINTS: PR00433; IL6CSFPGF.
DR SMART: SM00126; IL6: 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER
SQ SEQUENCE 118 AA: 13712 MW: 38FF24AB8D70A219 CRC64:
SO

Query Match 53.4%: Score 47; DB 6; Length 118;
Best Local Similarity 57.9%: Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSFKEFLQSSIRALROM 19
DB 100 ILRLMDTDFQSLRAVGM 118
|||||:|||||:|

RESULT 11
O9MZ07 PRELIMINARY: PRT; 118 AA.
AC O9MZ07: 01-OCT-2000 (TRIMBLREL. 15; Created)
DT 01-OCT-2000 (TRIMBLREL. 15; Last sequence update)
DR 01-JUN-2001 (TRIMBLREL. 17; Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
IL-6.
CN Lepus townsendii (white-tailed jackrabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
CX NCBI_TaxID=81325;

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RN 11)
SQ SEQUENCE FROM N.A.
RC TISSUE=OVARY.
DR MEDLINE-20304414; PubMed-10943729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
*The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
European rabbit (Oryctolagus cuniculus).";
DR Cytokine.12:555-565(2000).
DR EMBL: AF161818; AAF6564.1.
DR PIR: P00489.1; IL6_MGF_GCSF.
DR PRINTS: PR00433; IL6CSFPGF.
DR SMART: SM00126; IL6: 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER
SQ SEQUENCE 118 AA: 13712 MW: 38FF24AB8D70A219 CRC64:
SO

Query Match 53.4%: Score 47; DB 6; Length 118;
Best Local Similarity 57.9%: Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSFKEFLQSSIRALROM 19
DB 100 ILRLMDTDFQSLRAVGM 118
|||||:|||||:|

RESULT 12
O9WV08 PRELIMINARY: PRT; 210 AA.
AC O9WV08: 01-NOV-1999 (TRIMBLREL. 12; Created)
DT 01-NOV-1999 (TRIMBLREL. 12; Last sequence update)
DR 01-JUN-2001 (TRIMBLREL. 17; Last annotation update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CX NCBI_TaxID=10036;
DR TISSUE=OVARY.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
*APA hamsters IL-6 partial cDNA.";
DR EMBL: AB028633; BAA/8766.1.
DR HSP: P05218; IL6_MGF_GCSF.
DR PIR: P00489.1; IL6_MGF_GCSF.
DR PRINTS: PR00433; IL6CSFPGF.
DR SMART: SM00126; IL6: 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER
SQ SEQUENCE 210 AA: 24060 MW: HD919ABE9913AB3 CRC64:
SO

Query Match 51.1%: Score 45; DB 11; Length 210;
Best Local Similarity 44.4%: Pred. No. 16;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSFKEFLQSSIRALROM 18
DB 192 ILALSERFLAVYRNSTQ 209
|||||:|||||:|

RESULT 13
O50219 PRELIMINARY: PRT; 344 AA.
AC O50219: 01-JUN-1998 (TRIMBLREL. 06; Created)
DT 01-JUN-1998 (TRIMBLREL. 06; Last sequence update)
DR 01-JUN-2001 (TRIMBLREL. 17; Last annotation update)

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DE HYPOTHEICAL 38.5 KDA PROTEIN.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
RN NCBI_TaxID=287;
DB 111
RP SEQUENCE FROM N.A.
RA STRAIN-ICBP-PA14;
RA Rahme I.G., Tan M.-W., Le L., Wong S., Tompkins R.G., Calderwood S.B.,
RA Ausubel F.M.;
RA Proc. Natl. Acad. Sci. U.S.A. 94:0-0(1997).
RN NCBI_TaxID=287;
DR EMBL:AF015171.1; GenBank:AF015171.1; EMBL/GenBank/DBS databases.
DR InterPro: IPR000847; Pfam: PF00126; HTH_1.1; HTH_LysR.
KW DNA-binding; Hypothetical protein; Transcription regulation.
SQ SEQUENCE 344 AA: 38528 MW: 04228A3F0C8D2F6 CRC64;

Query Match
Best Local Similarity 51.1%; Score 45; DB 2; Length 344;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 3 RSXKFFLOSSLRALRM 19
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DB 279 RSXKFFLOSSLRALRM 295

RESULT 14
O9PYT0
ID O9PYT0 PRELIMINARY; PRT: 427 AA.
AC O9PYT0;
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DR 01-JUN-2001 (TREMBLrel. 17; Last annotation update)
GN ORE114.
OS Xestia c-nigrum granulosis virus (Xncv) (Xestia c-nigrum
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OC NCBI_TaxID=51677;
RN NCBI_TaxID=51677;
RP SEQUENCE FROM N.A.
RA NCBI_TaxID=51677; PubMed=10502508.
RA Hayakawa T., Ko R., Okano K., Seng S.T., Goto C., Wada S.;
RT Virology 262:277-297(1999).
RL EMBL: AF162221; AA052228.1;
SQ SEQUENCE 427 AA: 49747 MW: DA3412C416207AC CRC64;

Query Match
Best Local Similarity 51.1%; Score 45; DB 12; Length 427;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 ILSXKFFLOSSLRALRM 18
|||||:||||:||||:
DB 206 ILSXKFFLOSSLRALRM 223

RESULT 15
O16111
ID O16111 PRELIMINARY; PRT: 588 AA.
AC O16111;
DT 01-JAN-1998 (TREMBLrel. 05; Created)
DT 01-JAN-1998 (TREMBLrel. 05; Last sequence update)
DR 01-JUN-2001 (TREMBLrel. 17; Last annotation update)
GN TEL (FRANKENT).
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Phyllophaga; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7244;
RN (1)
RP SEQUENCE FROM N.A.
RA TRANSPOSON-TELEMAR.
RC Yella U., Yella C.P., Hartl D.L., Lazovskaya E.R.;
RA Yella U., Yella C.P., Hartl D.L., Lazovskaya E.R.;
DR EMBL:AF009430.1; GenBank:AF009430.1; EMBL/GenBank/DBS databases.
DR Flybase: FBgn004144; Drosophila.
DR InterPro: IPR001878; Znf.CCHC.
DR SMART: SM00343; Znf.C2HC; 2.
FT NON-TER 588
SQ SEQUENCE 588 AA: 64680 MW: 46910BD1F44F6673 CRC64;

Query Match
Best Local Similarity 51.1%; Score 45; DB 5; Length 588;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 LRSXKFFLOSSLRALRM 19
|||||:||||:||||:
DB 249 LRSXKFFLOSSLRALRM 266

Search completed: December 19, 2001, 16:25:20
Job time: 545 sec

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: December 19, 2001, 16:20:58 ; Search time 78.52 Seconds
(without alignments)
5.445 Million cell updates/sec

Title: US-09-202-104a-3

Perfect score: 88

Sequence: 1 ILRSKFEPGSSRLALRQM 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued:Patents.AA.*

1: /cgn2.6/pdata/2/1aa/5A.COMB.pep.*
2: /cgn2.6/pdata/2/1aa/5B.COMB.pep.*
3: /cgn2.6/pdata/2/1aa/6A.COMB.pep.*
4: /cgn2.6/pdata/2/1aa/6B.COMB.pep.*
5: /cgn2.6/pdata/2/1aa/PCUTS.COMB.pep.*
6: /cgn2.6/pdata/2/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO	Score	Query Match	Length	DB ID	Description
1	88	100.0	163	2	US-08-716-317-10
2	88	100.0	163	2	US-08-716-317-15
3	88	100.0	164	1	US-08-318-193-60
4	88	100.0	167	1	US-08-246-47A-2
5	88	100.0	167	2	US-08-766-620-2
6	88	100.0	181	1	US-08-209-182C-4
7	88	100.0	181	5	PCT-US92-05612-4
8	88	100.0	181	1	US-08-009-973-1
9	88	100.0	183	1	US-08-567-047-2
10	88	100.0	184	1	US-08-693-182-2
11	88	100.0	184	2	US-08-567-048-2
12	88	100.0	184	2	US-08-945-529-10
13	88	100.0	184	2	US-08-945-529-2
14	88	100.0	184	2	US-08-945-529-10
15	88	100.0	184	2	US-08-945-529-10
16	88	100.0	184	2	US-08-945-529-10
17	88	100.0	184	2	US-08-945-529-10
18	88	100.0	184	4	US-08-149-101A-22
19	88	100.0	184	5	PCT-US94-12873-23
20	88	100.0	184	6	US-08-149-101A-22
21	88	100.0	185	1	US-07-918-181A-2
22	88	100.0	185	1	US-08-231-575-2
23	88	100.0	185	1	US-08-246-47A-5
24	88	100.0	185	2	US-08-716-317-7
25	88	100.0	185	2	US-08-766-620-5
26	88	100.0	185	5	PCT-US92-05612-2

28	88	100.0	185	5	PCT-US93-06928-2	Sequence 2, App1
29	88	100.0	185	6	5186931-2	Patent No. 5186931
30	88	100.0	185	1	US-07-532-070S-2	Sequence 2, App1
31	88	100.0	185	1	US-07-532-070S-2	Sequence 2, App1
32	88	100.0	185	1	US-07-532-070S-2	Sequence 2, App1
33	88	100.0	185	1	US-08-209-182C-2	Sequence 2, App1
34	88	100.0	185	1	US-08-165-301A-20	Sequence 2, App1
35	88	100.0	185	3	US-08-469-318-163	Sequence 13, App
36	88	100.0	185	3	US-08-469-318-163	Sequence 13, App
37	88	100.0	185	4	US-08-810-436-20	Sequence 20, App1
38	88	100.0	185	5	PCT-US94-14179-20	Sequence 20, App1
39	88	100.0	185	3	PCT-US93-01283-103	Sequence 103, App
40	88	100.0	185	3	US-08-149-101A-19	Sequence 19, App1
41	88	100.0	185	3	US-08-149-101A-19	Sequence 19, App1
42	88	100.0	192	4	US-08-149-101A-19	Sequence 19, App1
43	88	100.0	192	4	PCT-US94-12873-18	Sequence 18, App1
44	88	100.0	194	4	US-08-149-101A-18	Sequence 18, App1
45	88	100.0	194	5	PCT-US94-12873-18	Sequence 18, App1

ALIGNMENTS

RESULT 1
US-08-716-317-10
Sequence 10, Application US/08716317
Patent No. 5919654
GENERAL INFORMATION:
APPLICANT: TOSHIDA, HIROKO
APPLICANT: TOSHIDA, HIROKO
APPLICANT: TSUKAMOTO, HIROKO
APPLICANT: NIKAIKO, KIYOKAZU
APPLICANT: KUMAGAI, HIROMICHI
TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
TITLE OF INVENTION: VECTOR CONTAINING IT
NUMBER OF SEQUENCES: 35
NUMBER OF SEQUENCES: 35
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P. C.
CITY: ARLINGTON
CITY: ARLINGTON
CITY: ARLINGTON
COUNTRY: USA
PCT NO: 01-FEB-1996
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08716-317
FILING DATE: 02-FEB-1996
CLASSIFICATION: A15
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY: NORMAN F.
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24, 618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INSTRUMENT CHARACTERISTICS: 10:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-716-317-10

Query Match 100.0%; Score 88; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 5.5e-07; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Indels 0;

OY 1 IIRSKREFLOSSIRALQM 19

DB 144 IIRSKREFLOSSIRALQM 162

RESULT 2

US-08-716-317-15

Sequence 15; Application US/08716317

Patent No. 5918654

GENERAL INFORMATION: YUKO

APPLICANT: TONDA, HIDEKI

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: NIKAIKO, KIYOKAZU

APPLICANT: KUMAGAI, HIROMICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

TITLE OF INVENTION: VECTOR CONTAINING IT

CORRESPONDENCE ADDRESS: 35

ADDRESSER: OBLON, SPIVAK, MCQUELLAND, MILER & NEUSTADT,

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-716-317-15

Query Match 100.0%; Score 88; DB 2; Length 163;

Best Local Similarity 100.0%; Pred. No. 5.5e-07; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Indels 0;

OY 1 IIRSKREFLOSSIRALQM 19

DB 145 IIRSKREFLOSSIRALQM 163

RESULT 3

US-08-318-193-60

Sequence 60; Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.

APPLICANT: MALEK, Lawrence E.

TITLE OF INVENTION: OR BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: ALBANY

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/07/935,314

FILING DATE: 07/22/96

ATTORNEY/AGENT INFORMATION:

NAME: BERT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 18740/116 CACO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)936-3800

TELEFAX: 8991491863-9109

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-318-193-60

Query Match 100.0%; Score 88; DB 1; Length 164;

Best Local Similarity 100.0%; Pred. No. 5.6e-07; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Indels 0;

OY 1 IIRSKREFLOSSIRALQM 19

DB 146 IIRSKREFLOSSIRALQM 164

RESULT 4

US-08-246-427A-2

Sequence 2; Application US/08246427A

Patent No. 5641657

GENERAL INFORMATION:

APPLICANT: RIBEN, ET AL.

TITLE OF INVENTION: Interleukin-6 Splice Variant

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: CARELLA, BYRNE, BAIN, GUILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2 MS-DOS
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,427A
 FILING DATE: Submitted herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: 08/246,427
 APPLICATION NUMBER: 435
 FILING DATE: MAY 19, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1700
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-246-427A-2

Query Match 100.0%; Score 88; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5,7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILNSKFFLOSSLALROM 19
 DB 149 ILNSKFFLOSSLALROM 167

RESULT 5
 US-08-766-620-2
 Sequence 2, Application US/08766520
 Patent No. 5058400
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice Variant
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2 MS-DOS
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,620
 FILING DATE: December 12, 1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 19, 1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-766-620-2

Query Match 100.0%; Score 88; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5,7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILNSKFFLOSSLALROM 19
 DB 149 ILNSKFFLOSSLALROM 167

RESULT 6
 PCT-US95-06094-2
 Sequence 2, Application PC/TUS9506094
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice Variant
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA: PC/TUS95/06094
 FILING DATE: Submitted herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 19, 1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 36,134
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 PCT-US95-06094-2

Query Match 100.0%; Score 88; DB 5; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5,7e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILNSKFFLOSSLALROM 19

DB 149 IIRSFKEFLQSSIRALQK 167

RESULT 7

US-08-209-182C-4
Sequence 4, Application US/08209182C
Patent No. 5545537
GENERAL INFORMATION:
APPLICANT: SKELLY, SUSAN M.
APPLICANT: SKELLY, CHARLES T.
APPLICANT: SNOWWELL, JOHN N.
APPLICANT: FOWLES, DANA M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutelins
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: 180 Varlick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-MAR-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/724,698
FILING DATE: 02-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: N. 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-209-182C-4

Query Match 100.0%; Score 88; DB 1; Length 181;

Best Local Similarity 100.0%; Pred. No. 6.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 163 IIRSFKEFLQSSIRALQK 181

RESULT 8

PCT-US92-05612-4
Sequence 4, Application PC/US9205612
GENERAL INFORMATION:
APPLICANT: SKELLY, SUSAN M.
APPLICANT: SKELLY, CHARLES T.
APPLICANT: SNOWWELL, JOHN N.
APPLICANT: FOWLES, DANA M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutelins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: 180 Varlick Street
CITY: New York
STATE: New York

COUNTRY: United States
ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 1992/07/02
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05612
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05612-4

Query Match 100.0%; Score 88; DB 5; Length 181;

Best Local Similarity 100.0%; P-red. No. 6.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 163 IIRSFKEFLQSSIRALQK 181

RESULT 9

US-08-009-973-1
Sequence 1, Application US/08009973
Patent No. 5538183
GENERAL INFORMATION:
APPLICANT: WILLIAMS, ASHLEY M.
TITLE OF INVENTION: Ultrapure Human Interleukin-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
CITY: Washington, D.C.
STATE: N.M., Suite 500
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,973
FILING DATE: 1993/01/26
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 1677/199 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)572-5300
TELEFAX: (202)572-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-08-009-973-1

Query Match 100.0%; Score 88; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ILISKEFLOSSALRQW 19
 |||||

DB 166 ILISKEFLOSSALRQW 183

RESULT 10
 US-08-567-047-2
 Sequence 2, Application US/08567047
 Patent No. 5789552
 Patent No. 5789552 5789555
 GENERAL INFORMATION:
 APPLICANT: SAVINO, Rocco
 APPLICANT: LAHW, Armin
 TITLE OF INVENTION: METHOD AND APPARATUS FOR SELECTING SUPERAGONISTS
 TITLE OF INVENTION: ANTAGONISTS AND SUPERAGONISTS FOR HORMONES HAVING
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 04-DEC-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/387,924
 FILING DATE: 23-FEB-1993
 APPLICATION NUMBER: US 08/393,000/409
 FILING DATE: 23-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: SAVINO-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 NO. OF SEQUENCES: 1
 MEDIUM TYPE: protein
 US-08-567-047-2

Query Match 100.0%; Score 88; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ILISKEFLOSSALRQW 19
 |||||

DB 166 ILISKEFLOSSALRQW 184

RESULT 11
 US-08-693-182-2

Sequence 2, Application US/08693182
 Patent No. 5849383
 GENERAL INFORMATION:
 APPLICANT: CLIBERTO, Genaro
 APPLICANT: SAVINO, Rocco
 APPLICANT: LAHW, Armin
 TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
 TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPERANTAGONISTS OF HUMAN
 TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
 TITLE OF INVENTION: MODELING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Browdy and Neimark, P.L.L.C.
 STREET: 419 Seventh Street N.W., Ste. 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/693,182
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PC/IT/95/00216
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IT RM 94A00805
 FILING DATE: 14-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: CLIBERTO-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-693-182-2

Query Match 100.0%; Score 88; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ILISKEFLOSSALRQW 19
 |||||

DB 166 ILISKEFLOSSALRQW 184

RESULT 12
 US-08-567-048-2
 Sequence 2, Application US/08567048
 Patent No. 5849398
 GENERAL INFORMATION:
 APPLICANT: SAVINO, Rocco
 APPLICANT: LAHW, Armin
 TITLE OF INVENTION: METHOD AND APPARATUS FOR SELECTING SUPERAGONISTS
 TITLE OF INVENTION: ANTAGONISTS AND SUPERAGONISTS FOR HORMONES HAVING
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 08/08/1995, 048
 FILING DATE: 04-DEC-1995
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/387,924
 FILING DATE: 23-FEB-1995
 APPLICATION NUMBER: IT RM93A000409
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.,
 REGISTRATION NUMBER: 25,618
 TELEPHONE: 202-628-5197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-737-3528
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-367-048-2

Query Match 100.0%; Score 88; Db 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6, 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFKEFLSSRLALQW 19
 DB 166 ILRSKFKEFLSSRLALQW 184

RESULT 13

US-09-008-482-2
 Sequence 2, Application US/09008482
 Patent No. 5972902
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: CILIBERTO, Gennaro
 APPLICATION: SAVINO, Rocco
 APPLICANT: LAHM, Armin
 TITLE OF INVENTION: A METHOD FOR SELECTING
 SUPERGENES, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
 TITLE OF INVENTION: SUPERGENES, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
 TITLE OF INVENTION: MODELLING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Browdy and Neimark, P.L.L.C.
 STREET: 419 Seventh Street N.W., Ste. 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 09/09/08, 482

FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 08/693,182
 FILING DATE: 14-AUG-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/IT95/00216
 FILING DATE: 13-DEC-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: IT RM 94A000805
 ATTORNEY/AGENT INFORMATION:
 NAME: YUN, Allen C.
 REGISTRATION NUMBER: 37,971
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (402) 628-5197
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-008-482-2

Query Match 100.0%; Score 88; Db 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6, 3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFKEFLSSRLALQW 19
 DB 166 ILRSKFKEFLSSRLALQW 184

RESULT 14

US-08-945-529-8
 Sequence 8, Application US/08945529
 Patent No. 5972902
 PRIORITY APPLICATION DATA:
 APPLICATION: CILIBERTO, Gennaro
 APPLICANT: SAVINO, Rocco
 APPLICANT: PIONESE, Giacomo
 TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
 TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: BROWDY AND NEIMARK, P.L.L.C.
 STREET: 419 Seventh Street N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/945,529
 FILING DATE: 26-OCT-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: IT RM95A000273
 FILING DATE: 28-APR-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/IT96/00084
 FILING DATE: 26-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: YUN, Allen C.
 REGISTRATION NUMBER: 37,971
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (402) 628-5197
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-008-482-2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQUENCE CHARACTERISTICS: 8:
 LENGTH: 184 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-945-529-8

Query Match 100.0% Score 88: DB 2: Length 184;
 Best Local Similarity 100.0% Pred. No. 6.3e-07;
 Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ILSKKEFTQSSIRALRM 19
 DB 166 ILSKKEFTQSSIRALRM 184

RESULT 15

US-08-945-529-9
 Sequence 9, Application US/08945529
 Patent No. 5972902
 GENERAL INFORMATION:
 INVENTOR: CLAUDIO GEMARRO
 APPLICANT: SAVITO KOCOMO
 APPLICANT: PIONEER, GILCOMO
 TITLE OF INVENTION: ANTICONSISTS OF HUMAN INTERLEUKIN-6 THAT
 TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWN AND NEWMARK, P.L.L.C.
 STREET: 415 South Street N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/945,529
 FILING DATE: 28-OCT-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: TM RM95A000273
 FILING DATE: 28-APR-1995
 APPLICATION NUMBER: PCT/IT96/00084
 FILING DATE: 26-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: YUN, Allen C
 REGISTRATION NUMBER: 37,971
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-945-529-9

Query Match 100.0% Score 88: DB 2: Length 184;
 Best Local Similarity 100.0% Pred. No. 6.3e-07;
 Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 ILSKKEFTQSSIRALRM 19
 DB 166 ILSKKEFTQSSIRALRM 184

Search completed: December 19, 2001, 16:20:59
 Job time: 40s sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:34 ; Search time 170.68 Seconds
(without alignments)
6.510 Million cell updates/sec

Title: US-09-202-104A-4
Sequence: 1 QLSGFRKSLSNVVC 15

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Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 10% summaries

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5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
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7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
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20: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
21: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	80	100.0	315	20	AAW07805
3	80	100.0	315	21	AAV92200
4	80	100.0	323	10	AAV90527
5	80	100.0	325	21	AAV13359
6	80	100.0	325	21	AAV13359
7	80	100.0	344	10	AAV90528
8	80	100.0	345	21	AAV55071
9	80	100.0	360	20	AAW07804
10	80	100.0	360	21	AAV92199
11	80	100.0	386	10	AAV90526

12	80	100.0	419	20	AAV30938
13	80	100.0	468	10	AAV90525
14	80	100.0	468	10	AAV90284
15	80	100.0	468	14	AAK37225
16	80	100.0	468	19	AAV71371
17	80	100.0	468	19	AAV71371
18	80	100.0	468	21	AAV92196
19	80	100.0	468	22	AAV36655
20	80	100.0	477	21	AAV92197
21	80	100.0	515	18	AAV36847
22	80	100.0	515	21	AAV15404
23	80	100.0	525	16	AAV35846
24	80	100.0	532	20	AAV70797
25	80	100.0	532	20	AAV70797
26	80	100.0	592	21	AAV92185
27	80	100.0	690	21	AAV92185
28	80	100.0	1042	16	AAV70122
29	80	100.0	1158	21	AAV92205
30	80	100.0	1168	21	AAV92204
31	71	89.8	182	17	AAV07403
32	62	73.9	460	12	AAK13138
33	62	77.5	460	13	AAK22656
34	62	77.5	460	22	AAV98475
35	62	77.5	460	22	AAV98475
36	43	53.8	215	22	AAV98479
37	43	53.8	215	22	AAV98481
38	43	53.8	215	22	AAV98481
39	42	52.5	311	18	AAV34550
40	42	52.5	311	18	AAV34550
41	42	52.5	861	16	AAV17658
42	42	52.5	861	19	AAV56540
43	42	52.5	861	22	AAV81035
44	42	52.5	861	22	AAV81035
45	41	51.2	216	22	AAV98466

ALIGNMENTS

RESULT	ID	AAW52204	standard; peptide: 15 AA.
1	XX	AAW52204:	
09-JUN-1998	XX	(first entry)	
Interleukin-6 antagonist peptide.	XX		
Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma; acquired immune deficiency syndrome-related lymphoma; immune response; rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy.	KW		
Alzheimer's disease.	KW		
Synthetic.	OS		
Human sapiens.	OS		
MO9748728-A1.	PN		
24-DEC-1997.	PN		
19-JUN-1997:	XX	97MC-NL00345.	
20-JUN-1996:	PF	96EP-0201720.	
(KOSTY) KOSTER H W.	PA		
Hoebe KIN, van Leengoed LMKG.	XX		
WPI: 1998-063080/06.	XX		
New peptide(s) with interleukin-6 agonist or antagonist activity -	DR		
useful for treatment, prevention and diagnosis of IL-6 associated	PT		

CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specifically determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization. The
CC beta-receptor is a heterodimeric complex composed of first the receptor
CC (IL-6R-alpha) and the extracellular domain of the receptor (IL-6R-beta).
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the absence of the ligand, the alpha-receptor and the beta-receptor
CC consisting of the ligand, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC beta-receptor. The heterodimers are useful for treating cytokine-related
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

Sequence 315 AA:

Query Match 100.0%; Score 80; DB 21; Length 315;
Best Local Similarity 100.0%; Pred. No. 3, 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCTFRKSPLSNVVC 15
|||||
DB 118 qlacitfrksplsnvvc 132

RESULT 4

AAp90527 standard; Protein: 323 AA.

AC AAp90527;

DX 25-JAN-1990 (first entry)

DE B cell stimulating factor-2 receptor.

KW B cell stimulating factor-2 receptor; monocytic U937 cell line.

OS Homo sapiens.

PN AU9828720-A.

PD 27-JUL-1989.

XX 23-JAN-1989; 89AU-0028720.

XX 23-JAN-1988; 88JP-0012387.

PR 25-JAN-1988; 88JP-0012589.

PR 04-AUG-1988; 88JP-0134885.

PR 14-JAN-1989; 89JP-0007461.

XX (KISH) TADMITSU KISHIMOTO.

PA Kishimoto T;

PI NPI. 1989-264032/37.

DR N-PSDB: AAP90525.

XX Receptor protein for human B cell stimulating factor-2 - used for

PT developing prophylactic, therapeutic and diagnostic agents for

PT associated disorders.

XX Claim 6; page 39; 76pp. english.

XX The BSP2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate to
CC the BSGF2 receptor. The BSGF2 receptor is a heterodimeric complex
CC study an immune mechanism with which BSP-2 or the receptor is concerned.

Sequence 323 AA:

Query Match 100.0%; Score 80; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 3, 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCTFRKSPLSNVVC 15
|||||
DB 118 qlacitfrksplsnvvc 132

RESULT 5

AA15389 standard; Protein: 325 AA.

AC AA15389;

DX 11-DEC-2000 (first entry)

DE Human Interleukin 6 receptor protein.

KW Human Interleukin-6 receptor; fungus; Pichia pastoris; PCR primer;

expression vector; immunoglobulin-like region; cytokine receptor region.

OS Homo sapiens.

PN JP2000157280-A.

PD 13-JUN-2000.

XX 26-NOV-1998; 98JP-0335464.

XX 26-NOV-1998; 98JP-0335464.

PR 26-NOV-1998; 98JP-0335464.

XX (TOXJ) TOSOH CORP.

PA NPI. 2000-468203/41.

PI N-PSDB: AA170701.

XX Yeasts transformed with IL-6 receptor gene -

Example 1; Page 6-8; 10pp; Japanese.

XX The invention relates to the production of human interleukin-6 receptor
CC (IL-6R) protein in the fungus Pichia pastoris. The fungus was
CC transformed with an expression vector (pGIC9-A20L) containing a gene
CC encoding an IL-6R protein having an immunoglobulin-like region and
CC cytokine receptor region and spanning amino acids from Leu370-A1a323. The
CC human IL-6R region was PCR amplified using the primers AA170702-A170703.
CC This sequence represents the recombinant IL-6R protein of the invention.

Sequence 325 AA:

Query Match 100.0%; Score 80; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 3, 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  OLSCRKSPISNVVC 15
        |||
Db      99  qlscfrkspisnvvc 113

RESULT 6
AA15390
AC      AAB15390 standard; Protein: 325 AA.
AC      AAB15390;
DX      15-DEC-2000 (first entry)
DX      Bovine Interleukin-12 p35 subunit protein.
DX      Antimicrobial; bovine; Interleukin 12; IL12; heterodimer; infection.
XX      Bos taurus.
XX      JP2000157274-A.
PD      13-JUN-2000.
PD      20-NOV-1998; 98JP-0331052.
PR      20-NOV-1998; 98JP-0331052.
PA      (DAUC ) DAITCH PHARM CO LTD.
DR      WPI; 2000-468201/41.
DR      N-PSDB; AAA70708.
PT      Preparation of bovine interleukin 12 comprising using a vector
PT      containing the gene encoding it; useful for the prevention and
PT      treatment of chronic and opportunistic infections -
XX      treatment of chronic and opportunistic infections.
PS      Example 1; Page 8; 11pp; Japanese.

XX      The invention relates to a method for the preparation of bovine
CC      interleukin 12 (boli12). boli12 consists of a heterodimer of p35
CC      and p40 subunits. The p35 subunit is encoded by a 308 bp cDNA
CC      fragment. The p40 subunit is encoded by a 350 bp cDNA fragment.
CC      Recombinant vectors containing the p35 and p40 subunits.
CC      This sequence represents the bovine IL12 p35 subunit. Interleukin 12
CC      is used for the prevention and treatment of chronic infections and
CC      opportunistic infections.
CC      Sequence 325 AA:
QY      1  OLSCRKSPISNVVC 15
        |||
Db      99  qlscfrkspisnvvc 113

RESULT 7
AAP9528
AC      AAP9528 standard; protein: 344 AA.
AC      AAP9528;
XX      25-JAN-1990 (first entry)
DX      B cell stimulating factor-2 receptor.
DX      B cell stimulating factor-2 receptor.
XX      B cell stimulating factor-2 receptor; monocyte U937 cell line.
XX      Homo sapiens.

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```

PN  A08928720-.A.
PD
PR  27-JUL-1989.
PX
PY  23-JAN-1989; 89AN-0028720.
PZ
XX
PR  22-JAN-1988; 88JP-0012387.
PR  25-JAN-1988; 88JP-0012599.
PR  04-AUG-1988; 88JP-0194885.
PR  14-JAN-1989; 89JP-0007461.
PX
PY  (KISH ) TADAMITSU KISHIMOTO.
PZ
XX
PI  Kishimoto T;
DR
XX  WPI; 1989-264012/37.
DR  N-PSDB; AAF90555.
PX
PY  Receptor protein for human B cell stimulating factor-2 - used for
PT  cloning of cDNA; therapeutic and diagnostic agents for
PT  associated disorders.
PX
PS  Claim 7: page 40; 76pp. English.
SQ
XX
PY  The BSE2 receptor has amino acids at the C-terminal deleted. The receptor
CC  is derived from a monocytic U937 cell line. It can be used to develop
CC  prophylactic and therapeutic pharmaceuticals, as agents to relate
CC  diseases and disorders to abnormal BSE2 protein. It can also be used to
CC  study an immune mechanism with which BSE-2 or the receptor is concerned.
XX
PY  Sequence 344 AA;
SQ
XX
PY  Query Match 100.0%; Score 80; DB 10; Length 344;
PY  Best Local Similarity 100.0%; Match No. 3,9e+06;
PY  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
PY  1 0LSCFRKSPISMWNC 15
PY  |||||
DB  118 qlacfkfksplsnvc 132
RESUT
R
R055071
R055071
R055071 standard; Protein; 345 AA.
AC
XX  AAY55071;
XX
XX  25-FEB-2000 (first entry)
XX
DE  SR345 protein sequence.
DE
XX  Gene isolation; membrane-bound protein; fusion protein; drug production;
XX  antigen-binding cell; secretible functional protein; antigenic protein;
XX  protein isolation; diagnostics; SR345 protein.
XX
XX  Homo sapiens.
OS
XX  M09960113-A1.
PN
XX  25-NOV-1999.
PD
XX
PF  30-APR-1999; 99MO-JP0241.
PF
XX
PR  20-MAY-1998; 98JP-0138652.
PR  01-OCT-1998; 98JP-0279876.
PX
PY  (CHUS ) CHUGAI SEIYAKU KK.
XX
XX
XX  Tsuchiya M, Saito M, Ohtomo T;
PI
XX  WPI; 2000-039382/03.
DR
XX  N-PSDB; AA240288.

```


XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 CC production of drugs treating abnormal functions of the protein -

Example 1; Page 49-52; 120pp; Japanese.

CC This sequence represents the SR345 protein.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC fusing the DNA, the vector contains DNA encoding a secretable DNA
 CC fused to the antigen, with a second vector which encodes a protein
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TMT) method
 CC protein.

SO Sequence 345 AA:

Query Match 100.0%; Score 80; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3; 9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCKRSPSLSNVC 15
 |||||
 DB 118 qlsckrpslsnvc 132

RESULT 9

ID AAW70804
 XX AAW70804 standard; protein: 360 AA.

AC AAW70804;

DT 03-FEB-1999 (first entry)

XX Amino acid sequence of the interleukin (IL)-6R-alpha domain.

XX gp130; cytokine antagonist; interleukin; gamma-interferon;

XX granulocyte macrophage colony-stimulating factor; J peptide;

XX transforming growth factor-beta.

OS Synthetic.

XX Key Location/Qualifiers

XX Protein 1 345
 FT /note= "soluble interleukin (IL)-6R-alpha domain"

XX US5844099-A.

XX 01-DEC-1998.

XX 27-NOV-1995; 9505-0563105.

XX 27-NOV-1995; 9505-0563105.

XX 20-OCT-1993; 9305-0140222.

XX (REG-) REGENERON PHARM INC.

XX Economides A, Stahl N, Yancopoulos GD;

XX WPI: 1999-044669/04.

XX Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 XX cytokine receptor

PS Example 4; Fig 15; 46pp; English.

CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha domain. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the receptor and the signal-transducing component of the cytokine
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and also are used in assays for identifying novel agonists and
 CC antagonists of cytokines.

SO Sequence 360 AA:

Query Match 100.0%; Score 80; DB 20; Length 360;
 Best Local Similarity 100.0%; Pred. No. 4; 1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCKRSPSLSNVC 15
 |||||
 DB 118 qlsckrpslsnvc 132

RESULT 10

ID AAY92199
 XX AAY92199 standard; protein: 360 AA.

AC AAY92199;

DT 01-AUG-2000 (first entry)

XX Soluble human IL-6-R-alpha.

XX Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor;

XX fusion protein; cytosolic; immunomodulator; osteopathic.

XX Homo sapiens.

XX WC200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99NO-US22045.

XX 25-SEP-1998; 98US-0101858.

XX 19-MAY-1999; 99US-0313942.

XX (REG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI: 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 CC to form a nonfunctional complex

XX Example 4; Fig 15; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component. The intermediate then binds to the
 CC soluble alpha specificity determining component of the receptor.
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the

ID AAP90525 standard; protein: 468 AA.
 AC AAP90525;
 DM 23-JAN-1990 (first entry)
 XX B cell stimulating factor-2 receptor.
 DE B cell stimulating factor-2 receptor.
 XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
 KW Homo sapiens.
 OS Homo sapiens.
 XX A08928720-A.
 XX 27-JUL-1989.
 PD 23-JAN-1989; 89AU-0028720.
 XX 22-JAN-1988; 88JP-0012387.
 PR 23-JAN-1988; 88JP-0012387.
 PR 04-APR-1993; 88JP-0012599.
 PR 14-JAN-1989; 89JP-0007461.
 XX (KISH) TADAMITSU KISHIMOTO.
 PA Kishimoto T;
 PI WPI: 1989-264012/37.
 DM N-PSDB; AAN90525.
 XX Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 XX Claim 2; page 36; 76pp; english.
 PS The BSH2 receptor is derived from a monocytic U937 cell line. It can be
 XX used to develop prophylactic and therapeutic pharmaceuticals as well as to
 CC relate diseases and disorders to abnormal BSH-2 protein. It can also be
 CC used to study an immune mechanism with which BSH-2 or the receptor is
 CC concerned.
 CC
 XX Sequence 468 AA;
 SQ
 Query Match 100.0%; Score 80; DB 10; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5; Se-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QLSCEKSPSLSNVC 15
 DB 118 qlscfrkspslsnvc 132
 RESULT 14
 AAP90284
 ID AAP90284 standard; Protein: 468 AA.
 AC AAP90284;
 DM 31-MAR-1992 (first entry)
 XX Sequence of a receptor protein for human B cell stimulating
 DE factor-2 (BSF2 receptor).
 XX B cell; Immune disorder; therapy; diagnosis; prophylaxis.
 KW Homo sapiens.
 OS Homo sapiens.
 XX Key
 FH Region 2...22 Location/Qualifiers
 FT Region /label= hydrophobic region
 FT Region 362..386

FT EP325474-A. /label= hydrophobic region
 XX 26-JUL-1989.
 PD 20-JAN-1989; 89EP-0300536.
 XX 14-JAN-1989; 89JP-0017461.
 PR 22-JAN-1988; 88JP-0012387.
 PR 25-JAN-1988; 88JP-0012599.
 PR 04-APR-1993; 88JP-0194885.
 PR 20-JAN-1989; 89JP-0009774.
 XX (KISH/) KISHIMOTO T.
 PA Kishimoto T;
 PI WPI: 1989-214667/30.
 DM N-PSDB; AAN90340.
 XX Receptor protein for human B cell stimulating factor-2 - obtd. by
 PT recombinant DNA techniques and used as diagnostic, prophylactic or
 PT therapeutic agent
 XX Claim 2; Page 19-21; 63pp; English.
 PS The cDNA in AAN90340 was derived from monocytic cell line U937.
 CC Isolated BSH2 receptor and DNA encoding it are claimed, as are
 CC (e) monoclonal antibodies; (c) host organisms; (d) antibodies; and
 CC (e) hybridomas.
 XX Sequence 468 AA;
 SQ
 Query Match 100.0%; Score 80; DB 10; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5; Se-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QLSCEKSPSLSNVC 15
 DB 118 qlscfrkspslsnvc 132
 RESULT 15
 AAR37215
 ID AAR37215 standard; Protein: 468 AA.
 AC AAR37215;
 DM 13-SEP-1993 (first entry)
 XX IL-6 receptor.
 DE IL-6 receptor.
 KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;
 KW disease; Intracellular.
 OS Synthetic.
 XX JP05091892-A.
 DM 16-APR-1993.
 PD 02-OCT-1991; 91JP-0255521.
 PR 02-OCT-1991; 91JP-0255521.
 PR (CHUS) CHUGAI PHARM CO LTD.
 PA (KISH/) KISHIMOTO C.
 PA (TOYJ) TOSOH CORP.
 XX WPI: 1993-161739/20.

DR N-PSDB; AAQ41746.
XX New interleukin-6 receptor deriv. - for treating diseases caused
PT by IL-6, e.g. multiple myeloma
XX
PS Disclosure: Page 10-12: 23pp; Japanese.
XX
CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
CC of the receptor lacking either the immunoglobulin-like domain or the
CC transmembrane and intracellular domain have IL-6 binding ability and
CC are capable of inducing biological responses. The IL-6 binding ability
CC receptors may be used for diseases caused by IL-6 such as multiple
CC myeloma.
XX
SQ Sequence 468 AA:

Query Match 100.0%; Score 80; DB 14; Length 468;
Description: Similarity 100.0%; Pos. No. 5; Se-0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QLSCFRKSPLSNVVC 15
|||||
DB 118 qlscfkrksplsnvvc 132

Search completed: December 19, 2001, 16:19:34
Job time: 359 sec

F:387-468/Domain: Intracellular status predicted <INT>
 F:47-96/Disulfide bonds: status predicted
 F:55-93/221,245,350/Binding site: carboxylate (Asn) (covalent) status predicted

Query Match 100.0%; Score 80; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 3,9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 QJSCFRKSPSLNVC 132

Query Match 100.0%; Score 80; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 3,9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 QJSCFRKSPSLNVC 132

RESULT 2

JU0144

Interleukin-6 receptor precursor (clone lambda p1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Accession: J010144 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
 R:Single, T.: Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A:Title: Functional murine interleukin 6 receptor with the intracellular a particle gen
 A:Reference number: JU0144; MUID:90278354
 A:Accession: JU0144
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: mRNA
 A:Residues: 1-440 <SIG>
 A:Cross-references: GB:X51976; NID:953548; PIDN:CAA6238.1; PID:953549
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-13/Domain: signal sequence status predicted <SIG>
 F:14-94/Domain: intracellular receptor status predicted <INT>
 F:40-94/Domain: intracellular receptor status predicted <INT>
 F:117-305/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane status predicted <TRA>

Query Match 77.5%; Score 62; DB 2; Length 440;
 Best Local Similarity 66.7%; Pred. No. 0.0048; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

Query Match 77.5%; Score 62; DB 2; Length 440;
 Best Local Similarity 66.7%; Pred. No. 0.0048; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

RESULT 3

JU0145

Interleukin-6 receptor precursor (clone lambda 301) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
 C:Accession: JU0145; S14543
 R:Single, T.: Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A:Title: Functional murine interleukin 6 receptor with the intracellular a particle gen
 A:Reference number: JU0145; MUID:90278354
 A:Accession: JU0145
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: mRNA
 A:Residues: 1-460 <SIG>
 A:Cross-references: GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
 A:Experimental source: clone lambda 301
 A:Keywords: cytokine receptor; transmembrane protein
 A:Submitted to the EMBL database: 1990
 A:Description: Cloning and expression of murine IL-6 receptor.
 A:Reference number: S14543
 A:Accession: S14543
 A:Molecule type: mRNA
 A:Residues: 1-373; R:375-460 <TR>
 A:Cross-references: EMBL:X53802; NID:953662; PIDN:CAA37810.1; PID:953693
 C:Superfamily: cytokine receptor; transmembrane protein; cytokine receptor; Immunog

C:Keywords: cytokine receptor; transmembrane protein
 F:1-13/Domain: signal sequence status predicted <SIG>
 F:14-94/Domain: intracellular receptor status predicted <INT>
 F:40-94/Domain: intracellular receptor status predicted <INT>
 F:117-305/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane status predicted <TRA>

Query Match 77.5%; Score 62; DB 2; Length 460;
 Best Local Similarity 66.7%; Pred. No. 0.005; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

Query Match 77.5%; Score 62; DB 2; Length 460;
 Best Local Similarity 66.7%; Pred. No. 0.005; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

RESULT 4

AJ7986

Interleukin-6 receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C:Accession: AJ7986
 R:Brumann, M.; Saumann, H.; Rey, G.H.
 J. Biol. Chem. 268, 19653-19662, 1993
 A:Title: Molecular cloning, characterization and functional expression of the rat IL-6
 A:Reference number: AJ7986; MUID:91060602
 A:Accession: AJ7986
 A:Molecule type: mRNA
 A:Residues: 1-462 <BAID>
 A:Cross-references: GB:M85897; GB:J05668; NID:9204921; PIDN:AAA1431.1; PID:9204922
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: acute phase; cytokine receptor; transmembrane protein
 F:1-13/Domain: signal sequence status predicted <SIG>
 F:14-94/Domain: intracellular receptor status predicted <INT>
 F:20-462/Product: interleukin-6 receptor status predicted <EXT>
 F:40-94/Domain: immunoglobulin homology <IMH>
 F:117-305/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane status predicted <TRA>
 F:386-462/Domain: intracellular status predicted <INT>
 F:47-92/Disulfide bonds: status predicted

Query Match 72.5%; Score 58; DB 1; Length 462;
 Best Local Similarity 66.7%; Pred. No. 0.024; 3; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

Query Match 72.5%; Score 58; DB 1; Length 462;
 Best Local Similarity 66.7%; Pred. No. 0.024; 3; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 114 KJSCFRKPNLVNVC 128

RESULT 5

AJ7986

Heat shock protein 26, chloroplast - wood tobacco (fragment)
 C:Species: Nicotiana glauca (wood tobacco)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: U15044
 R:Rice, B.H.; Tanaka, Y.; Iwasaki, T.; Yamamoto, N.; Kayano, T.; Miyao, M.
 Plant Mol. Biol. 37, 1035-1043, 1999
 A:Title: Evolutionary origin of two genes for chloroplast small heat shock protein of
 A:Accession: U15044; S14543; MUID:9616565
 A:Reference number: S14543
 A:Accession: S14543
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-205 <LEB>
 A:Cross-references: EMBL:AB006043; NID:9325377; PIDN:BA29066.1; PID:93256378
 A:Experimental source: green leaf
 A:Keywords: heat shock
 A:Submitted to the EMBL database: 1996
 A:Description: nuclear

RESULT 15

767971

hypothetical protein

```

c:species: Caenorhabditis elegans
c:date: 20-Sep-1999 #sequence_revision 20-Sep-1999
c:text_change 20-Sep-1999

```

R; Pauley, A.

submitted to the EMBL Data Library, July 1995

A; Description: The sequence of C. elegans cosmid F32A5.

A; reference number: 210402
A; revision: 016333

A;Status: preliminary: tra

A: Molecule type: DNA

A:Residues: 1-977 <P>

A; Cross-references: EMB

A;Experimental source: strain Bristol N2

C;Genetics:

A:Gene: CESP:F32A5.2

A; Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2

Query Match	Score	DB	Length
48.8%	39	2	977

BEST LOCAL SIMILARITY 33.38; Pred. NO. 9

malines 0; consilvalve 2; mismalines 3; indels 0; gaps 0;

QY 1 QLSCEFKSPISNVC 15

Db 948 QVEIRKSSLRITC 962

Search completed: December 19, 2001, 16:22:37
Job time: 457 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:14 ; Search time 48.45 Seconds
(without alignments)
11,351 Million cell updates/sec

Title: us-09-202-104a-4
Sequence: 1 QUSCFRSPLENTYC 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	468	1 IL6A_HUMAN	P08887 homo sapien
2	73	91.2	467	1 IL6A_HUMAN	O18786 mus scrofa
3	72	91.2	467	1 IL6A_HUMAN	P22222 mus muscu
4	72	91.2	467	1 IL6A_HUMAN	P22222 mus muscu
5	42	52.5	861	1 SMD_MOUSE	O05126 ratu
6	42	52.5	861	1 SMD_MOUSE	O05126 ratu
7	41	51.2	1818	1 Z294_HUMAN	O09966 caenorhabd
8	40	50.0	356	1 CBM5_CAEEL	O04822 homo sapien
9	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
10	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
11	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
12	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
13	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
14	39	48.8	430	1 MS12_CGARR	P78003 mycoplasma
15	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
16	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
17	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
18	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
19	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
20	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
21	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
22	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
23	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
24	38	47.5	161	1 K793_CAEEL	P34320 caenorhabd
25	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
26	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
27	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
28	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
29	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
30	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
31	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
32	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus
33	37	46.2	157	1 SMG_BACVI	P17176 oryctolapus

34	37	46.2	2820	1 NEI_RAT	P97526 ratu
35	37	46.2	2839	1 NEI_HUMAN	P21359 homo sapien
36	37	46.2	2841	1 NEI_MOUSE	O04650 mus muscu
37	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
38	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
39	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
40	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
41	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
42	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
43	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
44	36	45.0	118	1 P22222_MOUSE	O10112 lactuca
45	36	45.0	118	1 P22222_MOUSE	O10112 lactuca

ALIGNMENTS

RESULT	1	IL6A_HUMAN	STANDARD:	PRT:	468 AA.
1	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
2	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
3	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
4	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
5	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
6	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
7	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
8	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
9	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
10	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
11	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
12	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
13	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
14	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
15	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
16	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
17	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
18	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
19	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
20	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
21	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
22	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
23	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
24	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
25	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
26	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
27	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
28	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
29	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
30	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
31	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
32	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	
33	IL6A_HUMAN	STANDARD:	PRT:	468 AA.	

RN SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE-LIVER;
 RC 1-IL-6; Mattern R.L.;
 RC Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC -see also EMBL accession no. Z11666).
 CC -----
 CC EMBL: AF147881; AAF73109.1; -;
 CC EMBL: AF015116; AAB70916.1; -;
 CC HSSP: P16471; IBP3.
 CC InterPro: IPR002996; CRIA.
 CC InterPro: IPR001777; FN.III.
 CC InterPro: IPR003530; Hematopo_receptor_L_F3.
 CC InterPro: IPR003598; IL6C2.
 CC Pfam: PF00047; fn3.1.
 CC Pfam: PF00047; lg.1.
 CC SMART: SM00060; FN3.1.
 CC SMART: SM00408; ICG2.1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC Signal.
 CC FT SIGNAL 1 19
 CC FT DOMAIN 20 467
 CC FT TRANSMEM 20 365
 CC FT DOMAIN 366 386
 CC FT DOMAIN 387 467
 CC FT DOMAIN 407 103
 CC FT DISULFID 25 193
 CC FT DISULFID 121 133
 CC FT DISULFID 165 176
 CC FT CARBOHYD 55 55
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 221 221
 CC FT CARBOHYD 350 350
 CC FT SPOUNCE 467 AA; 51066 MW; A2B08645F21502 CRC64;
 SQ
 Query Match 91.2%; Score 73; DB 1; Length 467;
 Best Local Similarity 93.3%; Pred. No. 8-9e-06;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AC P2272;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 CC Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases
 CC TISSUE-LIVER;
 CC -1- FUNCTION: RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 CC MUS musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 CC (1)
 CC SEQUENCE FROM N.A.
 CC SPOUNCE FROM N.A.
 CC MEDLINE=00278354; PubMed=2111585;
 CC SUGITA T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
 CC Kishimoto T.;
 CC Functional murine interleukin 6 receptor with the intracellular A
 CC particle gene product at its cytoplasmic domain. Its possible role in
 CC plasmacytogenesis;
 CC J. Exp. Med. 171:2001-2009(1990).
 CC -----
 CC SEQUENCE FROM N.A.
 CC SPOUNCE FROM N.A.
 CC STRAIN=C3H; TISSUE=Liver;
 CC Fiorillo M.T., Ciliberto G., Dente L.;
 CC Submitted (JUL-1990) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -see also EMBL accession no. Z11666).
 CC -----
 CC EMBL: X51975; CA936237.1; -;
 CC EMBL: X53802; CA937810.1; -;
 CC PIR: J10144; J10144.
 CC PIR: J10145; J10145.
 CC PIR: S15431; S15431.
 CC WMD: MG1105304; IL6R.
 CC InterPro: IPR002996; CRIA.
 CC InterPro: IPR001777; FN.III.
 CC InterPro: IPR003530; Hematopo_receptor_L_F3.
 CC InterPro: IPR003006; IL6C2.
 CC InterPro: IPR003598; IL6C2.
 CC Pfam: PF00047; fn3.1.
 CC Pfam: PF00047; lg.1.
 CC SMART: SM00060; FN3.1.
 CC SMART: SM00408; ICG2.1.
 CC PROSITE: PS01354; HEMATOPO_REC_L_F3.1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC Signal.
 CC FT SIGNAL 1 19
 CC FT DOMAIN 20 467
 CC FT TRANSMEM 20 364
 CC FT DOMAIN 365 385
 CC FT DOMAIN 386 460
 CC FT DOMAIN 40 99
 CC FT DISULFID 25 190
 CC BY SIMILARITY.

FT	DISULFID	47	92		BY SIMILARITY.
FT	DISULFID	117	128		BY SIMILARITY.
FT	DISULFID	162	173		BY SIMILARITY.
FT	CARRIWD	52	32		N-LINKED (GLCNC..)
FT	CARRIWD	52	32		POTENTIAL).
FT	CARRIWD	150	150		N-LINKED (GLCNC..)
FT	CARRIWD	150	150		POTENTIAL).
FT	CONFLICT	374	374		A -> R (IN REF. 2.)
SO	SEQUENCE	460 AA:	5045A MW:	F85C5906D8525C4	CHRC64;
Query Match	Best Local Similarity	66.7%	Score 62,	DB 1:	Length 460;
Matches 10;	Conservative	3;	Pred. No. 0.00060;		Gaps 0;
Oy	1 QLSCKRSPSLWVC 15		Mismatches 2;	Indels 0;	Gaps 0;
Db	114 KLSCKRNPVLVAVIC 128				
RESULT 4					
ID	IL6A.PAT	STANDARD:	PTT:	462 AA.	
AC	P2273;				
DT	01-AUG-1991 (Ref. 1), Created				
DT	01-FEB-1995 (Ref. 3), Last sequence update)				
DE	20-MAY-2001 (Ref. 40, Last annotation update)				
DY	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R-1).				
OS	Rattus norvegicus (Rat)				
OC	Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
NCBI_Taxid=10116;					
RN	(1)				
RP	SEQUENCE FROM N.A.				
RS	SIMILARITY SCORES: 14.7 MISRE-ALIGN:				
RL	SHAW, D.; SHAW, J. H.; SHAW, M. L.; SHAW, S. L.; SHAW, T. A.; SHAW, W. B.; SHAW, Y. C.; SHAW, Z. L.; SHAW, A. A.; SHAW, B. A.; SHAW, C. H.; SHAW, D. G. H.; SHAW, E. H.; SHAW, F. H.; SHAW, G. H.; SHAW, H. H.; SHAW, I. H.; SHAW, J. H.; SHAW, K. H.; SHAW, L. H.; SHAW, M. H.; SHAW, N. H.; SHAW, O. H.; SHAW, P. H.; SHAW, Q. H.; SHAW, R. H.; SHAW, S. H.; SHAW, T. H.; SHAW, U. H.; SHAW, V. H.; SHAW, W. H.; SHAW, X. H.; SHAW, Y. H.; SHAW, Z. H.; SHAW, A. A.; SHAW, B. A.; SHAW, C. A.; SHAW, D. A.; SHAW, E. A.; SHAW, F. A.; SHAW, G. A.; SHAW, H. A.; SHAW, I. A.; SHAW, J. A.; SHAW, K. A.; SHAW, L. A.; SHAW, M. A.; SHAW, N. A.; SHAW, O. A.; SHAW, P. A.; SHAW, Q. A.; SHAW, R. A.; SHAW, S. A.; SHAW, T. A.; SHAW, U. A.; SHAW, V. A.; SHAW, W. A.; SHAW, X. A.; SHAW, Y. A.; SHAW, Z. A.; SHAW, A. B.; SHAW, B. B.; SHAW, C. B.; SHAW, D. B.; SHAW, E. B.; SHAW, F. B.; SHAW, G. B.; SHAW, H. B.; SHAW, I. B.; SHAW, J. B.; SHAW, K. B.; SHAW, L. B.; SHAW, M. B.; SHAW, N. B.; SHAW, O. B.; SHAW, P. B.; SHAW, Q. B.; SHAW, R. B.; SHAW, S. B.; SHAW, T. B.; SHAW, U. B.; SHAW, V. B.; SHAW, W. B.; SHAW, X. B.; SHAW, Y. B.; SHAW, Z. B;				
RT	rat liver Interleukin 6 receptor.*				
RT	J. Biol. Chem. 265:19853-19863(1990).				
RU	[2]				
RV	IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.				
RL	Unpublished observations (Feb-1995).				
CC	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6, BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOIESIS.				
CC	-1- SUBUNIT: DIMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY ANALOGY).				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- DOMAIN: THE TWO FIBROECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 3 FIBROECTIN TYPE III-LIKE DOMAINS.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
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CC	EMBL: X72987, AF7966.				
DR	HSP: P16471, IAP3.				
DR	InterPro: IPRO02996; CRA.				
DR	InterPro: IPRO01177; FN.III.				
DR	InterPro: IPRO03530; Hematoctoprot.L.F3.				
DR	InterPro: IPRO03006; IG_MHC.				

DR	InterPro: IPRO03598; Ig_C2.
DR	Pfam: PF00041; Fc3_1.
DR	Sfrmr: SFRM0047; 19; 1; 1.
DR	SMART: SM00060; FN3_1
DR	PROSITE: PS00354; HEIMATOPOI_REC_L_F3_1.
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW	Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN,
FT	EXTRACELLULAR (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN
FT	DISULFID
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	DISULFID
FT	N-LINKED (GLNMC...) (POTENTIAL).
FT	CARBOHYD
FT	N-LINKED (GLNMC...) (POTENTIAL).
FT	CARBOHYD
FT	N-LINKED (GLNMC...) (POTENTIAL).
FT	XPRHLKSMQPPSSDSVYLLOFDLRLRWNSXK ->
FT	CONFLICT
FT	SLVSKSVGKTLSPGVGYTCCTCSNPSFDLYGGRT
FT	(IN REP. 1).
SO	SEQUENCE
SC	462 AA; 50398 MW; AD05064CDD0337D CRC64;
QY	Query Match
Dy	Best local similarity 66.7%; Score 58; Db 1; Length 462;
Dy	Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Dy	1 QLSRKSPLSNVC 15
Dy	114 KLSGRNPDPANEC 128
RESULT 5	
SM4D_MOUSE	STANDARD; PRT; 861 AA.
ID	SM4D_MOUSE
AC	009126; (Ref. 1, Created)
DT	30-MAY-2000 (Ref. 1, Last sequence update)
DE	20-AUG-2001 (Ref. 40, Last annotation update)
DE	SEMAPHORIN 4D PRECURSOR (SEMAPHORIN J) (SMA J) (SEMAPHORIN C-LIKE 2)
DE	(K-SEVA G).
GN	SEMA4 OR SEMA4 OR SEMA4C2.
OS	Mus musculus (mouse)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OC	NCBI_TaxID=10090.
RP	SEQUENCE FROM N.A.
RX	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=97125976; PubMed=8969198;
RA	Furuyama T., Miyazaki N., Kosugi A., Node S., Satoh S.-I., Ogata M.,
RA	Iwanishi Y., Iwazaki N., Hamano T., Toyama H.;
RA	Identification of a novel transmembrane semaphorin expressed on
RA	J. Biol. Chem. 271:33376-33381(1996).
RL	-1 FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL
CC	AS IN THE NERVOUS SYSTEM.
CC	-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1 TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPOID TISSUES,
CC	ESPECIALLY IN THE THYMUS, AS WELL AS IN THE NERVOUS TISSUES.
CC	-1 SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC	-1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration
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CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way


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RL Nature 405:311-319(2000).
RP SEQUENCE OF 707-1818.
RC TISSUE-BRAIN.
RA MEDLINE-99087487; PubMed-9872452.
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RA *Prediction of the coding sequences of unidentified human genes. XI.
RA The complete sequences of 100 new cDNA clones from brain which code
RA for large proteins (1998).
RL DNA RANGE: 572338-1998.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: STRONG, TO YEAST YER44C.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
DR EMBL: AL163249; CAB90430.1;
DR EMBL: AL163249; CAB90429.3;
DR EMBL: AB018225; BA04484.1;
DR UNIPROT: P50067; GPROTEIN.B;
DR SMART: SM00184; RING, 1.
RW ZINC-FINGER.
FT ZN-FING 1767 1813 RING-TYPE.
SO SEQUENCE 1818 AA; 205732 MW; 416B387DADACA705 CRC64;

Query Match 51.28; Score 41; DB 1; Length 1818;
Best local Similarity 57.18; E-Val NO. 23;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

DY 2 LSCFRKSPISNYVC 15
DB 634 LSPURKKPLEDAVC 647
||| ||| ||| |||

RESULT 8
GBBS.CABEL STANDARD; PRT; 356 AA.
AC Q20636;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DR P23946 NCICLONIDE-BINDING PROTEIN BETA SUBUNIT 5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditia; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCB1_TaxID=6239;
FN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALST01 N2.
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GINATINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC EFFECTOR ACTIVITY. FOR REPLACEMENT OF GTP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1- SIMILARITY: PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 AND REPEATS (PSP-1) (CALYX).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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DR EMBL: 271263; CA95824.1;
DR HSSP: P04901; 1MG.
DR Wormpep: F52A8.2; CE17845.
DR InterPro: IPR001632; Gprotein.B.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR000319; GPROTEINB.
DR PROSITE: PS00678; WD_REPEATS_REGION.
DR PROSITE: PS00678; WD_REPEATS-2; 3.
DR PROSITE: PS00678; WD_REPEATS-2; 5.
DR PROSITE: PS00678; WD_REPEATS-2; 1.
RW Transducer; Repeat; WD repeat; Multigene family.
FT REPEAT 66
FT REPEAT 108 138 WD 2
FT REPEAT 138 158 WD 3
FT REPEAT 158 178 WD 4
FT REPEAT 196 228 WD 4
FT REPEAT 240 270 WD 5
FT REPEAT 284 314 WD 6
FT REPEAT 326 356 WD 7
SO SEQUENCE 356 AA; 39453 MW; 293A0DCE31D832 CRC64;

Query Match 50.08; Score 40; DB 1; Length 356;
Best local Similarity 46.78; E-Val NO. 6.4;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

DY 1 QLSCFKSPISNYVC 15
DB 330 RLSCLRTSPDSTAVC 344
||| ||| ||| |||

RESULT 9
METK.MYCPN STANDARD; PRT; 383 AA.
AC P78003;
DT 01-NOV-1997 (Rel. 35, Created)
DT 20-AUG-2001 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 35, Last annotation update)
DR S11000 NCICLONIDE-BINDING PROTEIN BETA SUBUNIT 5.1(6) (METHIONINE.
DR ADENOSITRANSFERASE) (ADONET SYNTHETASE).
OS METK OR METX OR MPN060 OR MP094.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
NCB1_TaxID=2104;
FN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-ATCC 29342 / M129.
RX MEDLINE-97105885; PubMed-6948693;
RA Himmelfeich R., Hilbert H., Pletsch E., Li B.-C.,
RA Hermann R.;
RA *Complete sequence analysis of the genome of the bacterium Mycoplasma
RA pneumoniae.
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- FUNCTION: ANALYZES THE REGULATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O -> ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL.
CC -1- SIMILARITY: BELONGS TO THE ADONET SYNTHETASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC EMBL: A8000011: AAB95742.1:
DR BSSP: P04384: IXRC.
DR InterPro: IPR002133: S-ADOMET_synth.
DR PROSITE: PS00376: ADOMET_SYNTHETASE.1.1.
DR PROSITE: PS00377: ADOMET_SYNTHETASE.2.1.
DR TRANSFERASE: One-carbon metabolism: ATP-binding: complete proteome.
FT NP_BIND 114 119 ATP (POTENTIAL).
SQ SEQUENCE 383 AA: 42560 MW: 655817BAF4E65051 CRC64:

Query Match
Best Local Similarity 50.0%: Score 40. DB 1: Length 383;
Matches 6: Conservative 3; Mismatches 3; Indels 0; Gaps 0:

OY 4 CFFKSPISNWC 15
DB 38 CIKSPISNWC 49

RESULT 10
MS12.AGRH STANDARD: PRT: 430 AA.
AC P50201:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 40, Last annotation update)
DE AGROPLINE SYNTHESIS REDUCTASE (EC 1.1.1.17).
MA SI
OS Agrobacterium rhizogenes.
OC Plasmid pRi8196.
CC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group:
CC Rhizobiaceae: Rhizobium.
CC NCBI_Taxid=359:
XX
RP SEQUENCE FROM N.A.
RA MEDLINE:9132070: PubMed:1909028;
RA Hansen G., Larriba M., Vaubert D., Tempe J., Blermann B.J.,
RA Montoya A.L., Chilton M.D., Brevet J.:
RA Agrobacterium rhizogenes pRi8196 T-DNA: mapping and DNA sequence of
RA functions involved in mannopine synthesis and hairy root
RA formation. Plant Cell Tissue Organ Cult. 66:17-26 (2001).
RT Proc Natl Acad Sci U S A. 88:7763-7767(1991).
CC -1- FUNCTION: REDUCES DEOXY-FRUCTOSE-6-PHOSPHATE TO MANNOPINE.
CC -1- PATHWAY: AGROPLINE / MANNOPINE SYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SD) FAMILY.
XX
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CC or send an email to license@isb-sib.ch).
XX
CC Entry: 10090: AAA22101.1:
DR BSSP: P14061:
DR InterPro: IPR002199: ADH_short.
DR InterPro: IPR001345: PG_mutase.
DR Pfam: PF00106: adh_short.1.
DR Pfam: PF00300: PGAM.1.
DR PROSITE: PS00061: ADH_SHORT.1.
DR Pfam: P00061: ADH_SHORT.1.
XX
CC Pfam: OX1010: OX1010.
CC Pfam: OX1010: OX1010.
XX
CC NBD OR NBD (BY SIMILARITY).
FT ACT_SITE 346 346
FT ACT_SITE 346 346
FT ACT_SITE 346 346
XX
SQ SEQUENCE 430 AA: 47583 MW: D01B7EBD2654DCC CRC64:

Query Match
Best Local Similarity 70.0%: Score 39. DB 1: Length 430;
Matches 7: Conservative 2; Mismatches 1; Indels 0; Gaps 0:

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OY 6 RKSPISNWC 15
DB 70 RKLPISNWC 79

RESULT 11
CC48.CAPAN STANDARD: PRT: 805 AA.
ID CC48.CAPAN
AC 096372:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELL DIVISION CYCLE PROTEIN 48 HOMOLOG.
CN CNP.
OS Capsicum annuum (Bell pepper).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: eusterids I: Solanales: Solanaceae: Capsicum.
XX
CC NCBI_Taxid=4072:
XX
RP SEQUENCE FROM N.A.
RA STRAIN-CV. YELLOW WONDER: TISSUE-FRUIT:
RA Akim S., Houine G., Schantz M.L., Schantz R.:
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PROBABLY FUNCTIONS IN CELL DIVISION AND GROWTH
CC PROCESSES.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
XX
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL database.
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CC or send an email to license@isb-sib.ch).
XX
CC Entry: Y09396: CAA70565.1:
DR InterPro: IPR003593: AAA.
DR InterPro: IPR001938: AAA_subfam.
DR Pfam: PF00044: AAA_2.1.
DR Pfam: PF00044: AAA_2.1.
DR SMART: SM00382: YAAH2.
DR PROSITE: PS00674: AAA_2.
DR Cell cycle: ATP-binding: Repeat.
FT NP_BIND 249 256 ATP (POTENTIAL).
FT NP_BIND 522 529 ATP (POTENTIAL).
SQ SEQUENCE 805 AA: 89331 MW: 58E975F8E266AD CRC64:

Query Match
Best Local Similarity 77.8%: Score 39. DB 1: Length 805;
Matches 7: Conservative 1; Mismatches 1; Indels 0; Gaps 0:

OY 3 CFFKSPIS 11
DB 663 ACLKSPIS 671

RESULT 12
HD.RAT STANDARD: PRT: 3110 AA.
ID HD.RAT
AC P51111:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HUNTINGTIN (HUNTINGTIN'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN).
GN HD.
OS Rattus norvegicus (Rat).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
XX
CC NCBI_Taxid=10116:

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Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 4 CRKSPSN 12
114
DB 104 CRKSPSPGN 112

Search completed: December 19, 2001, 16:26:15
Job time: 570 sec

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RESULT 2
DB 1 QUSCFKRSPLSNVC 15
ID 09N124 PRELIMINARY: PRT: 215 AA.
AC 09N124:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
SC 34.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Girol D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
RM EMBL: AF127898; AAF40291.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
FT NON_TER 1
FT NON_TER 215
FT SEQUENCE 215 AA; 23705 MW; FE073BC5BD712B9 CMC64;

Query Match
Best Local Similarity 53.8%; Score 43; DB 6; Length 215;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QUSCFKRSPLSNVC 15
DB 98 QUSCFKRSPLSNVC 112

RESULT 3
DB 1 QUSCFKRSPLSNVC 15
ID 09N120 PRELIMINARY: PRT: 215 AA.
AC 09N120:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
SC 34.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Girol D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
RM EMBL: AF127902; AAF40295.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
FT NON_TER 1
FT NON_TER 215
FT SEQUENCE 215 AA; 23663 MW; EAS670CF4DDC01B1 CMC64;

Query Match
Best Local Similarity 53.8%; Score 43; DB 6; Length 215;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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OY 1 QUSCFKRSPLSNVC 15
DB 98 QUSCFKRSPLSNVC 112

RESULT 4
DB 1 QUSCFKRSPLSNVC 15
ID 09N118 PRELIMINARY: PRT: 215 AA.
AC 09N118:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
SC 34.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Girol D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
RM EMBL: AF127899; AAF40292.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
FT NON_TER 1
FT NON_TER 215
FT SEQUENCE 215 AA; 23695 MW; FE073BC5BD711BA CMC64;

Query Match
Best Local Similarity 53.8%; Score 43; DB 6; Length 215;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QUSCFKRSPLSNVC 15
DB 98 QUSCFKRSPLSNVC 112

RESULT 5
DB 1 QUSCFKRSPLSNVC 15
ID 09KPK1 PRELIMINARY: PRT: 1436 AA.
AC 09KPK1:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN TC0424.
SC 34.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydia.
NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MOB9;
SC MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brumhan R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uitterlinden T., Berry K., Bass S.,
RA Linher K., Nelson M., Deboy R., Kolonay J., Bowman C., Dodson R.,
RA Gavin N., Nelson M., Deboy R., Kolonay J., Bowman C., Salzberg S.L.,
RP "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RP trachomatis AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL: AE002309; AAF9280.1;
DR TIGR: TC0424;
DR Hypothetical protein; Complete Proteome.
RM SEQUENCE 1436 AA; 161977 MW; F3CD01803DC287C CMC64;

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Query Match 53.8%; Score 43; DB 2; Length 1436;
Best Local Similarity 46.7%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 1 QUSCRKPSPLSNVC 15
:::1111:::
DB 771 EISSRRDPIDNLLC 785

RESULT 6
ID 077551 PRELIMINARY; PRT; 176 AA.
AC 077551;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Sus scrofa (pig).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suid.
NCBI_TaxID=9823;
[1]

SEQUENCE FROM N.A.
RA Matarazzo V., Tizard A., Renucci M., Belaich A., Clement J.L.;
RT Isolation of putative olfactory receptor sequences from pig nasal
RT epithelium (Jan-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF042026; MNC24802.1 -
DR Interpro: IPRO00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PSS0262; G_PROTEIN_RECPT-FL2; 1.
FT NON_TER 1 176
FT MON_TER 176 176
SQ SEQUENCE 176 AA; 19122 MW; A859CB3CE40B65F CRC64;

Query Match 53.5%; Score 42; DB 6; Length 176;
Best Local Similarity 46.7%; Pred. No. 3; 5; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 QUSCRKPSPLSNVC 15
:::1111:::
DB 50 QUSCRKPSPLSNVC 64

RESULT 7
ID 09001 PRELIMINARY; PRT; 263 AA.
AC 09001;
DT 01-MAR-2000 (TREMBLrel. 13, Created)
DT 01-MAR-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BC319430.5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Sellwagen S.,
RA Phan H., Velasco N., Do L., Beal A., Terry A., Garne J.,
RA Danghan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Atlix C., Andrieu T., Frankham M., Amco-Keller G., Coakfield J.,
RA Delpire E., Delpire E., Tanc B., Kottler B.,
RA Alencio A., Sanders C., Ow B., Nolan W., Tiong S., Kodajashi A.,
RA Olsen A.S., Carreno A.V.;
RT Sequence analysis of a 2.5 kb region in 19p13.2 between D19S461 and
PRKCSH.
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006271; AAD0353.1 -
DR Interpro: IPRO00276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PSS0262; G_PROTEIN_RECPT-FL2; 1.
SQ SEQUENCE 263 AA; 29791 MW; 16586C73601F3B9C CRC64;

Query Match 52.5%; Score 42; DB 4; Length 263;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 QUSCRKPSPLSNVC 15
:::1111:::
DB 107 QUSCRKPSPLSNVC 121

RESULT 8
ID 043789 PRELIMINARY; PRT; 264 AA.
AC 043789;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA TISSUE-TESTES:
RX MEDLINE-9745789; PubMed-9268701;
RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
RT Molecular cloning and chromosomal mapping of olfactory receptor genes
RT expressed in the male germ line: evidence for their wide distribution
RT in the human genome. Commun. 237:283-287(1997).
DR EMBL: X10529; AF071557.1 -
DR Interpro: IPRO00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PSS0262; G_PROTEIN_RECPT-FL2; 1.
KW G-protein coupled receptor.
FT NON_TER 1 264
FT MON_TER 264 264
SQ SEQUENCE 264 AA; 29888 MW; 43086CDD1BF3B10 CRC64;

Query Match 52.5%; Score 42; DB 4; Length 264;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 QUSCRKPSPLSNVC 15
:::1111:::
DB 108 QUSCRKPSPLSNVC 122

RESULT 9
ID 09014 PRELIMINARY; PRT; 402 AA.
AC 09014;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE)
(EC 2.5.1.6).
GN Mtr.
OS Plasmodium falciparum (Isolate 3D7), and
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
NCBI_TaxID=36329, 5833;
[1]
SEQUENCE FROM N.A.
RP SPECIES-P. falciparum (Isolate 3D7);
RC MEDLINE-20036339; PubMed-10567242;
RX

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL: X91022; CAAG62499.1; JOINED.

DR EMBL: X91022; CAAG62499.1; JOINED.

DR InterPro: IPR001039; MHC_I.

DR Pfam: PF00047; Ig; 1.

DR ProDom: PD000050; MHC_I; 1.

DR SMART: SM00407; IGH1.1.

DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.

DR NCBI: X91022; MHC; Transmembrane.

FT NON_TER 1

FT NON_TER 228

SEQUENCE 228 AA; 25817 MW; 6030DP0010A53076 CRC64;

Query Match

Best Local Similarity 51.2%; Score 41; DB 7; Length 228;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 QLSCKRSPSLSYVC 15

DB 95 QVSLDQKPLSLPYTC 109

RESULT 13

ID Q31387 PRELIMINARY; PRT; 348 AA.

AC Q31387

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

CS MHC CLASS I PROTEIN PRECURSOR.

CC Cyphilus carpio (Common carp).

OS Cyphilus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cyprinodontiformes; Cyprinidae; Cyprinus.

OX NCBI_TaxID:7962;

RN [1]

RP SEQUENCE FROM N.A.

RS SCHIZOSACCHAROMYCES pombe (Fission yeast).

RA MEDLINE:96217555; PubMed:8613142;

RA van Epp S.H., Dixon B., Figueroa F., Eports R., Spec R.J.;

RT Identification and characterization of a new major histocompatibility complex class I gene in carp (Cyphilus carpio L.).*

RL Immunogenetics 44:49-61(1996).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL: X91015; CAAG62497.1; *

DR InterPro: IPR003597; Ig_G1.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR001039; MHC_I.

DR Pfam: PF00047; Ig; 1.

DR ProDom: PD000050; MHC_I; 1.

DR SMART: SM00407; IGH1.1.

DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.

DR GlycoProtein: MHC; Signal; Transmembrane.

FT SIGNAL 1

FT SIGNAL 16

FT CHAIN 348 MHC CLASS I PROTEIN

SEQUENCE 348 AA; 39008 MW; 04163C972821AC CRC64;

Query Match

Best Local Similarity 51.2%; Score 41; DB 7; Length 348;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 QLSCKRSPSLSYVC 15

DB 199 QVSLDQKPLSLPYTC 213

RESULT 14

ID Q9NDV5 PRELIMINARY; PRT; 630 AA.

AC Q9NDV5

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

CS CDNA FL11053.F15 CLONE PLACED1004664 (FRAGMENT).

CC Homo sapiens (Human).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RS HAYASHI K., SUGIYAMA T., OTSUKI T., SUZUKI Y.,

RA IISOGAI T., OOTA T., HAYASHI K., SUGIYAMA T., OTSUKI T., SUZUKI Y.,

RA NISHIKAWA H., ISHII S., KAWAI Y., SAITO K., YAMANOJO J., MAKAMATSU A.,

RA NAKAMURA Y., NAGAHARI K., MASUHO Y., SASEKI N.

RT NEDO human cDNA sequencing project.*

RL Submitted (FE8-2000) to the EMBL/Genbank/DBJ databases.

FT NM_0001915; BH45376.1; *

FT NM_0001915; BH45376.1; *

SEQUENCE 630 AA; 71539 MW; C9C0B855180DE90 CRC64;

Query Match

Best Local Similarity 51.2%; Score 41; DB 4; Length 630;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 LSPFKRSPSLSYVC 15

DB 516 LSPFKRSPSLSYVC 529

RESULT 15

ID Q94275 PRELIMINARY; PRT; 807 AA.

AC Q94275

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

CS PUTATIVE UBQUITIN-PROTEIN LIGASE.

DE SPBP887.27.

CC Schizosaccharomyces pombe (Fission yeast).

OS Schizosaccharomyces pombe (Fission yeast); Schizosaccharomycetes; Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetes; Schizosaccharomycetes;

OX NCBI_TaxID:4896;

RN [1]

RP SEQUENCE FROM N.A.

RS BECK A., REINHARDT R., LYNE M., ROJANDREAN M.A., BARRELL B.G.;

RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

CS InterPro: IPR000569; HECT.

DR InterPro: IPR001607; zf-UBP.

DR InterPro: IPR001607; zf-UBP.

DR Pfam: PF00632; HECT; 1.

DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN.1.

DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN.1.

DR SMART: SM00135; HECT; 1.

DR SMART: SM00290; ZNF-UBP; 1.

FT LIGASE

SEQUENCE 807 AA; 93414 MW; 7203B2667E2DAB CRC64;

Query Match 51.2%; Score 41; DB 3; Length 807;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ISCFRKSPISN 12
:||||:|:|:
Db 288 ISCFRKQPYNN 298

Search completed: December 19, 2001, 16:25:21
Job time: 346 sec

GenCode version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:20:59 ; Search time 78.52 seconds
(without alignments)
4.299 Million cell updates/sec

Title: US-09-202-104a-4

Perfect score: 1 QUSCFKRSPLSNVC 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, AA:*

- 1: /cgn2.6/pdataa/2/1aa/5A.COMB.pep:*
- 2: /cgn2.6/pdataa/2/1aa/5B.COMB.pep:*
- 3: /cgn2.6/pdataa/2/1aa/6A.COMB.pep:*
- 4: /cgn2.6/pdataa/2/1aa/6B.COMB.pep:*
- 5: /cgn2.6/pdataa/2/1aa/6C.COMB.pep:*
- 6: /cgn2.6/pdataa/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	80	100.0	210	4 US-09-043-785-1	Sequence 1, Appl1
2	80	100.0	323	6 5171840-6	Patent No. 5171840
3	80	100.0	323	6 5480796-6	Patent No. 5480796
4	80	100.0	344	6 5171840-7	Patent No. 5171840
5	80	100.0	346	6 5480796-7	Patent No. 5480796
6	80	100.0	386	6 5480796-5	Patent No. 5171840
7	80	100.0	386	6 5480796-5	Patent No. 5171840
8	80	100.0	468	4 US-08-795-4735-5	Sequence 5, Appl1
9	80	100.0	468	6 5171840-40	Patent No. 5171840
10	80	100.0	468	6 5480796-2	Patent No. 5480796
11	67	83.8	188	1 US-07-676-647-8	Sequence 8, Appl1
12	67	83.8	188	1 US-08-449-329-8	Sequence 8, Appl1
13	67	83.8	188	1 US-08-443-073-8	Sequence 8, Appl1
14	67	83.8	188	1 US-08-443-073-8	Sequence 8, Appl1
15	67	83.8	188	1 US-08-443-073-8	Sequence 8, Appl1
16	62	65.0	201	6 PCT-US91-03896-8	Patent No. 5171840
17	39	48.8	318	2 US-08-457-2738-8	Sequence 6, Appl1
18	39	48.8	319	1 US-08-246-982A-16	Sequence 16, Appl1
19	39	48.8	319	1 US-08-453-285-16	Sequence 16, Appl1
20	39	48.8	319	1 US-08-246-982A-16	Sequence 16, Appl1
21	39	48.8	314	1 US-08-457-2738-8	Sequence 6, Appl1
22	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
23	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
24	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
25	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
26	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
27	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
28	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
29	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
30	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
31	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
32	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
33	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
34	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
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36	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
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41	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
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44	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1
45	39	48.8	314	2 US-08-457-2738-8	Sequence 6, Appl1

ALIGNMENTS

28	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
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32	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
33	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
34	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
35	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
36	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
37	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
38	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
39	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
40	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
41	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
42	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
43	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
44	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1
45	37	46.2	2485	5 PCT-US94-00196-2	Sequence 2, Appl1

US-09-043-785-1
Sequence 1, Application US/09043785

Patent No. 6172042

GENERAL INFORMATION: Juddih

APPLICANT: HANDBY, HUBERT

APPLICANT: REVEL, MICHEL

TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY

FILE REFERENCE: Chebath-1

CURRENT APPLICATION NUMBER: US/09/043-785

EARLIER APPLICATION NUMBER: PCT/IL96/00119

EARLIER FILING DATE: 1998-09-02

EARLIER APPLICATION NUMBER: 115,453

EARLIER FILING DATE: 1995-09-26

EARLIER APPLICATION NUMBER: 116,097

EARLIER FILING DATE: 1996-05-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 110

TYPE: PPT

ORGANISM: Human

US-09-043-785-1

Query Match

Best Local Similarity 100.0%; Pred. No. 5; be-07;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QUSCFKRSPLSNVC 15

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6 QUSCFKRSPLSNVC 20

RESULT 2

5171840-6

Patent No. 5171840

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA

FILING DATE: 19-JAN-1999

SEQ ID NO: 6

LENGTH: 323

5171840-6

Query Match 100.0%; Score 80; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
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 DB 118 QLSCFKRSPLSNVC 132

RESULT 3

Patent No. 5480796
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 STIMULATORY FACTOR-2
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION NUMBER: 298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 8;
 LENGTH: 323
 5480796-6

Query Match 100.0%; Score 80; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
 |||||||
 DB 118 QLSCFKRSPLSNVC 132

RESULT 4

Patent No. 5171840
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 7;
 LENGTH: 344
 5171840-7

Query Match 100.0%; Score 80; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
 |||||||
 DB 118 QLSCFKRSPLSNVC 132

RESULT 5

Patent No. 5480796
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 STIMULATORY FACTOR-2
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 298,694

FILING DATE: 19-JAN-1989
 SEQ ID NO: 7;
 LENGTH: 344
 5480796-7

Query Match 100.0%; Score 80; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
 |||||||
 DB 118 QLSCFKRSPLSNVC 132

RESULT 6

Patent No. 5171840
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 5;
 LENGTH: 386
 5171840-5

Query Match 100.0%; Score 80; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
 |||||||
 DB 36 QLSCFKRSPLSNVC 50

RESULT 7

Patent No. 5480796
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 STIMULATORY FACTOR-2
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 5;
 LENGTH: 386
 5480796-5

Query Match 100.0%; Score 80; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFKRSPLSNVC 15
 |||||||
 DB 36 QLSCFKRSPLSNVC 50

RESULT 8

US-08-795-473b-5
 Sequence 5, Application US/08795473b
 Patent No. 6217858
 GENERAL INFORMATION:
 APPLICANT: Galun, Elhan
 APPLICANT: Nahol, Ofit

```

; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; NUMBER OF SEQUENCES: 10
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA: Hepatitis B Virus (HBV) Infection
; FILING DATE: 02 JUL 1992
; PUBLICATION DATE: 02 JUL 1992
; ADDRESS: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,4738
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; NAME/AGENCY INFORMATION:
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-08-795-4738-5

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Query Match      100.0%; Score 80; DB 4; Length 468;
Best Local Similarity 100.0%; Pred No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QLSCKRSPSLSNVC 15
DB 118 QLSCKRSPSLSNVC 132

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RESULT 9
5171840-2
; PATENT NO. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2
; LENGTH: 468
; 5171840-2

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Query Match      100.0%; Score 80; DB 6; Length 468;
Best Local Similarity 100.0%; Pred No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QLSCKRSPSLSNVC 15
DB 118 QLSCKRSPSLSNVC 132

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RESULT 10
5480796-2
; PATENT NO. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

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; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02 JUL 1992
; PUBLICATION DATE: 02 JUL 1992
; ADDRESS: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,4738
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; NAME/AGENCY INFORMATION:
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-08-795-4738-5

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Query Match      100.0%; Score 80; DB 6; Length 468;
Best Local Similarity 100.0%; Pred No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QLSCKRSPSLSNVC 15
DB 118 QLSCKRSPSLSNVC 132

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RESULT 11
US-07-676-647-8
; Sequence 8, Application US/07/676647
; Patent No. 5426177
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; INVENTOR: Smith, Stephen P.
; APPLICANT: Yangopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,647
; FILING DATE: 19910328
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,982
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TEXELX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: AMINO ACIDS
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-07-676-647-8

```

```

Query Match      81.9%; Score 67; DB 11; Length 188;
Best Local Similarity 100.0%; Pred No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 CFKRSPSLSNVC 15
DB 118 CFKRSPSLSNVC 132

```


FILING DATE: 05/01/700, 6/77
 APPLICATION NUMBER: 05/01/700, 6/77
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOCK, S. Leslie
 REGISTRATION NUMBER: 18, 8/2
 REFERENCE/DOCKET NUMBER: 6526-0655
 TELEPHONE/CANADA TELEPHONE:
 TELEPHONE: 212 790-0050
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO.: 8
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 OS-MOL-585-258-8

Query Match	83.8%	Score 67	DB 2	Length 188
Best Local Similarity	100.0%	Pred. No. 0.00011		
Matches 12	Conservative 0	Mismatches 0	Indels 0	Gaps 0

RESULT 15
 PCT-US91-03896-8
 Sequence 8, Application, PC/TUS9103896
 GENINVENTOR: Sequence 8, Application, PC/TUS9103896
 APPLICANT: Davis, Samuel
 APPLICANT: Quinto, Stephen P.
 APPLICANT: Firth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 NUMBER OF SEQUENCES: 15
 ADDRESSER: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 19910603
 CLASSIFICATION: 439
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065-228
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO. 8:
 SOURCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 STRAIGHTNESS: single
 TOPOLOGY: unknown
 PCT-US91-03896-8
 MOLECULE TYPE: peptide

```

Query Match      83.88; Score 67; Db 5; Length 188;
Best Local Similarity 100.08; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CERSKSNVNC 15
        |||||
Db       1 CERSKSNVNC 12

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Search completed: December 19, 2001, 16:20:59
Job time: 404 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 19, 2001, 16:19:34 ; Search time 170.68 seconds

(without alignments) 8,680 Million cell updates/sec

Title: us-09-202-104a-6

Sequence: 1 MCVASSVSKRFTQTQGC 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 7407390 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: A.Geneseq.1101.*

1: /SIDSR/gcgdata/geneseq/AA1980.DAT.*

2: /SIDSR/gcgdata/geneseq/AA1981.DAT.*

3: /SIDSR/gcgdata/geneseq/AA1982.DAT.*

4: /SIDSR/gcgdata/geneseq/AA1983.DAT.*

5: /SIDSR/gcgdata/geneseq/AA1984.DAT.*

6: /SIDSR/gcgdata/geneseq/AA1985.DAT.*

7: /SIDSR/gcgdata/geneseq/AA1986.DAT.*

8: /SIDSR/gcgdata/geneseq/AA1987.DAT.*

9: /SIDSR/gcgdata/geneseq/AA1988.DAT.*

10: /SIDSR/gcgdata/geneseq/AA1989.DAT.*

11: /SIDSR/gcgdata/geneseq/AA1990.DAT.*

12: /SIDSR/gcgdata/geneseq/AA1991.DAT.*

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17: /SIDSR/gcgdata/geneseq/AA1997.DAT.*

18: /SIDSR/gcgdata/geneseq/AA1998.DAT.*

19: /SIDSR/gcgdata/geneseq/AA1999.DAT.*

20: /SIDSR/gcgdata/geneseq/AA2000.DAT.*

21: /SIDSR/gcgdata/geneseq/AA2001.DAT.*

22: /SIDSR/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	105	100.0	20	19	AAW2206	Interleukin-6 anta
2	105	100.0	183	17	AAW0403	Interleukin-6 anta
3	105	100.0	315	20	AAW0805	Antio acid sequenc
4	105	100.0	315	21	AAW2200	Soluble human IL-6
5	105	100.0	323	10	AAW0527	B cell stimulating
6	105	100.0	325	21	AAW1389	Human Interleukin
7	105	100.0	325	21	AAW1390	Human Interleukin
8	105	100.0	344	10	AAW0558	B cell stimulating
9	105	100.0	345	21	AAW55071	SH35 protein sequ
10	105	100.0	360	20	AAW0804	Antio acid sequenc
11	105	100.0	360	21	AAW92199	Soluble human IL-6

12	105	100.0	386	10	AAW0526	B cell stimulating
13	105	100.0	419	20	AAW0538	Human IL-6 receptor
14	105	100.0	468	10	AAW0525	B cell stimulating
15	105	100.0	468	10	AAW0528	Sequence of a rece
16	105	100.0	468	14	AAW27215	IL-6 receptor - sy
17	105	100.0	468	15	AAW1372	Human Interleukin
18	105	100.0	468	19	AAW1372	Human Interleukin
19	105	100.0	468	21	AAW2196	Human IL-6 receptor
20	105	100.0	468	22	AAW6555	Human IL-6 receptor
21	105	100.0	477	21	AAW92197	Human IL-6 receptor
22	105	100.0	500	18	AAW3647	Human IL-6 receptor
23	105	100.0	515	21	AAW15404	Human IL-6 receptor
24	105	100.0	523	20	AAW0534	Human IL-6 receptor
25	105	100.0	523	20	AAW0534	Human IL-6 receptor
26	105	100.0	592	20	AAW0797	Human IL-6 receptor
27	105	100.0	592	21	AAW92185	Human IL-6 receptor
28	105	100.0	690	21	AAW92195	Human IL-6 receptor
29	105	100.0	1042	16	AAW0712	Human IL-6 receptor
30	105	100.0	1158	21	AAW2205	Human IL-6 receptor
31	105	100.0	1168	21	AAW2205	Human IL-6 receptor
32	105	100.0	1168	21	AAW2205	Human IL-6 receptor
33	105	100.0	1168	21	AAW2205	Human IL-6 receptor
34	105	100.0	1168	21	AAW2205	Human IL-6 receptor
35	105	100.0	1168	21	AAW2205	Human IL-6 receptor
36	105	100.0	1168	21	AAW2205	Human IL-6 receptor
37	105	100.0	1168	21	AAW2205	Human IL-6 receptor
38	105	100.0	1168	21	AAW2205	Human IL-6 receptor
39	105	100.0	1168	21	AAW2205	Human IL-6 receptor
40	105	100.0	1168	21	AAW2205	Human IL-6 receptor
41	105	100.0	1168	21	AAW2205	Human IL-6 receptor
42	105	100.0	1168	21	AAW2205	Human IL-6 receptor
43	105	100.0	1168	21	AAW2205	Human IL-6 receptor
44	105	100.0	1168	21	AAW2205	Human IL-6 receptor
45	105	100.0	1168	21	AAW2205	Human IL-6 receptor

ALIGNMENTS

RESULT 1	
AAW2206	standard: peptide: 20 AA.
ID	
XX	AAW2206:
XX	
XX	09-JUN-1998 (first entry)
XX	
XX	Interleukin-6 antagonist peptide.
DE	
XX	Interleukin-6: IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW	acquired immune deficiency syndrome-related lymphoma; immune response;
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW	Alzheimer's disease.
OS	Synthetic.
XX	Hom sapiens.
XX	
XX	W09748728-A1.
XX	
XX	24-DEC-1997.
XX	
XX	19-JUN-1997: 97MO-NL00345.
PR	
XX	20-JUN-1996: 96EP-0201720.
XX	
XX	(KOST/) KOSTER H W.
XX	
XX	Hoeb KIN, van Leeengoed LAMG;
XX	
XX	WPI: 1998-063080/06.
XX	
XX	New peptide(s) with Interleukin-6 agonist or antagonist activity -
PT	useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 XX
 XX Claim 6; Page 17; 28pp; English.
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC disease, HIV/AIDS, Alzheimer's disease etc.) also to remove IL-6 or IL-6R
 CC from extracellular blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC immunogenic). They may also be used in combination with other agents, or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies (the mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 XX
 XX Sequence 20 AA:
 30
 Query Match 100.0%; Score 105; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MCVASSVGSFKSTQTGQC 20
 1 MCVASSVGSFKSTQTGQC 20
 1 MCVASSVGSFKSTQTGQC 20
 DB 1 MCVASSVGSFKSTQTGQC 20
 RESULT 2
 AAM00403 standard; peptide; 182 AA.
 XX
 XX AAM00403;
 XX
 DT 29-AUG-1996 (first entry)
 DE Interleukin-6 antagonist peptide.
 XX
 XX IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 PN JPO7324097-A.
 PD 12-DEC-1995.
 XX
 XX 30-MAY-1994; 94JP-0117259.
 XX
 XX 30-MAY-1994; 94JP-0117259.
 XX
 XX (DAIIL) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 XX WPI: 1996-065416/07.
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 XX Claim 1; Page 2; 19pp; Japanese.
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence 91AA, AAM00401, AAM00402, AAM00403 (the present sequence)
 CC or AAM00404, where any three methapso groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAM00428 - AAM00435) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 XX
 XX Sequence 182 AA:
 30
 Query Match 100.0%; Score 105; DB 17; Length 182;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MCVASSVGSFKSTQTGQC 20
 1 MCVASSVGSFKSTQTGQC 20
 1 MCVASSVGSFKSTQTGQC 20
 DB 73 MCVASSVGSFKSTQTGQC 92
 RESULT 3
 AAM00805 standard; protein; 315 AA.
 XX
 XX AAM00805;
 XX
 XX 03-FEB-1999 (first entry)
 DT
 XX Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
 XX
 XX gp130; cytokine antagonist; interleukin; gamma-interferon;
 XX granulocyte macrophage colony-stimulating factor; J peptide;
 XX transforming growth factor-beta.
 XX
 OS Synthetic.
 PN Key
 FT Key Location/Qualifiers
 FT Protein 1..313
 /note="truncated interleukin (IL)-6R-alpha domain"
 XX
 XX US5844099-A.
 XX
 XX 01-DEC-1998.
 XX
 XX 27-NOV-1995; 95US-0563105.
 XX
 XX 27-NOV-1995; 95US-0563105.
 XX
 XX 20-OCT-1993; 93US-0140222.
 XX
 XX (REGF-) REGENERON PHARM INC.
 XX
 XX Economides A, Stahl N, Yancopoulos GD;
 XX WPI: 1999-044669/04.
 XX
 XX Cytokine antagonists - comprising extracellular domains of
 XX specificity-determining and signal-transducing components of
 XX cytokine receptor
 XX
 XX Example 4; Fig 16; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
 CC invention. The specification describes cytokine antagonists comprising of
 CC the extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC specificity-determining component of the cytokine
 CC is an interleukin (IL)-1, IL-2, IL-3, IL-4, IL-5 or IL-15).
 CC gamma-interferon or transforming growth factor (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX
 XX Sequence 315 AA.

[illegible]

Cc		The cytokine inaccessible to form a signal transducing complex with the
Cc		active membrane bound forms of their receptor. The nucleic acids and
Cc		polypeptides are useful for treating cytokine-related diseases or
Cc		disorders such as osteoporosis and primary and secondary effects of
Cc		cancer including multiple myeloma or leukemia.
Cx		
S0	Sequence	315 AA:
Oy	Query Match	100.0%;
Oy	Best Local Similarity	100.0%;
Oy	Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MCYASNGSKSPKRGPGC 20	
Oy	192 mcvasngsksfakrtqfagc 211	
Db		
RESULT_5		
AAFP0527	AAFP0527 standard; protein; 323 AA.	
Xx	AAFP0527;	
Ac	25-JAN-1990 (first entry)	
Df	B cell stimulating factor-2 receptor.	
Xx	B cell stimulating factor-2 receptor.	
Xm	B cell stimulating factor-2 receptor; monocytic U937 cell line.	
Xx	Homo sapiens.	
Os	AU8928720-A.	
Pn	27-JUL-1989.	
Xx	23-JAN-1989; 89AC-0028720.	
Xf	22-JAN-1988; 88JP-0012387.	
Xx	PR 25-JAN-1988; 88JF-0012599.	
Pr	04-AUG-1988; 88JF-0194885.	
Pr	14-JAN-1989; 89JP-0007461.	
Xx	(KISH) TADAMITSU KISHIMOTO.	
Pa	Kishimoto T;	
Dr	WPI; 1989-264012/37.	
Dr	N-FSDB; AAP0525.	
Xx	Receptor protein for human B cell stimulating factor-2 - used for	
Pt	developing prophylactic, therapeutic and diagnostic agents for	
Pt	associated disorders.	
Ps	Claim 6; page 39; 76pp. english.	
Cc	The Bsf2 receptor has amino acids at the C-terminal deleted. The receptor	
Cc	is derived from a monocytic U937 cell line. It can be used to develop	
Cc	prophylactic and therapeutic pharmaceuticals, as agents to relate	
Cc	diseases and disorders to abnormal BSF-2 prodn. It can also be used	
Cc	to study an immune mechanism with which BSF-2 or the receptor is concerned.	
Xx		
S0	Sequence	323 AA:
Oy	Query Match	100.0%; Score 105; DB 10;
Oy	Best Local Similarity	100.0%; Pred. No. 5, 6e-09;
Oy	Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MCYASNGSKSPKRGPGC 20	
Oy	192 mcvasngsksfakrtqfagc 211	
Db		

RESULT 6
 AA015389 standard: Protein: 325 AA.
 AC AAB15389;
 DT 11-DEC-2000 (first entry)
 DE Human Interleukin 6 receptor protein.
 KM Human: interleukin-6 receptor; fungus: *Pichia pastoris*; PCR primer: expression vector; immunoglobulin-like region; cytokine receptor region.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FN MISC-difference /note= "encoded by GCG"
 FT MISC-difference 281 /note= "encoded by CMA"
 PT
 XX JP2000157280-A.
 XX 13-JUN-2000.
 XX 26-NOV-1998: 98JP-0335454.
 XX 26-NOV-1998: 98JP-0335454.
 XX (TOYO) TOSOH CORP.
 XX WPI: 2000-468203/41.
 XX N-PSDB: AAA70702.
 XX Yeasts transformed with IL-6 receptor gene -
 XX Example 1: Page 6-8; 10pp; Japanese.
 XX The invention relates to the production of human interleukin-6 receptor
 CC encoding an IL-6 receptor protein having an immunoglobulin-like region and
 CC transformed with an expression vector (pTOC9-A20IL6) containing a gene
 CC encoding an IL-6R protein and spanning amino acids from leu20-ala323. The
 CC cytokine receptor region and spanning amino acids from leu20-ala323. The
 CC human IL-6R region was PCR amplified using the primers AAA70702-A70703.
 CC This sequence represents the recombinant IL-6R protein of the invention.
 CC Sequence 325 AA:
 SQ
 Query Match 100.0%; Score 105; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 5; De-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 1 MCVASSVSGSKFSTQTPGCC 20
 DB 173 mcvassvsgskstqtlgtgqc 192
 RESULT 7
 AA015390 standard: Protein: 325 AA.
 AC AAB15390;
 DT 15-DEC-2000 (first entry)
 DE Bovine interleukin-12 p35 subunit protein.
 KM Antileukemic; bovine: interleukin 12; IL12; heterodimer; infection.
 OS Bos taurus.
 XX

FN JP2000157274-A.
 XX 13-JUN-2000.
 XX 20-NOV-1998: 98JP-0331052.
 XX 20-NOV-1998: 98JP-0331052.
 XX (DAUC) DAICHI PHARM CO LTD.
 XX WPI: 2000-468201/41.
 XX N-PSDB: AAA70708.
 XX Preparation of bovine interleukin 12 comprising using a vector
 PT containing the gene encoding it, useful for the prevention and
 FT treatment of chronic and opportunistic infections -
 XX Example 1: Page 8; 11pp; Japanese.
 CC The invention relates to a method for the preparation of bovine
 CC interleukin 12 (boil12). Boil12 consists of a heterodimer of p35
 CC and p40 subunits. Boil12 is produced by introducing into a host cell,
 CC recombinant vectors containing genes encoding the p35 and p40 subunits.
 CC This sequence represents the bovine IL12 p35 subunit. Interleukin 12
 CC is a cytokine involved in the regulation and treatment of chronic and
 CC opportunistic infections.
 CC Sequence 325 AA:
 SQ
 Query Match 100.0%; Score 105; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 5; De-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 1 MCVASSVSGSKFSTQTPGCC 20
 DB 173 mcvassvsgskstqtlgtgqc 192
 RESULT 8
 AA090528 standard: Protein: 344 AA.
 AC AAP90528;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KM B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 XX A08928720-A.
 XX 27-JUL-1989.
 XX 23-JAN-1989: 89AU-0028720.
 XX 22-JAN-1988: 88JP-0012387.
 XX 25-JAN-1988: 88JP-0012599.
 XX 04-AUG-1988: 88JP-0194885.
 XX 14-JAN-1989: 89JP-0007461.
 XX (KISH) TADAMITSU KISHIMOTO.
 XX Kishimoto T.
 XX WPI: 1989-264012/37.
 XX N-PSDB: AAP90525.
 XX Receptor protein for human B cell stimulating factor-2 - used for
 FT developing prophylactic, therapeutic and diagnostic agents for

[illegible]

RESULT	11
AAV92199	
ID	AAV92199 standard; protein; 360 AA

DT 01-AUG-2000 (first entry)

DE Soluble human IL-6-R- α .

KM Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor
KM fusion protein; cytostatic; immunomodulator; osteopathic.

OS Homo sapiens.

PN WO200018932-A2

PD 06-APR-2000

PF 22-SEP-1999; 99WO-US22045.

PR 25-SEP-1998; 98US-0101858 -
30-MAY-1999; 98US-0323043 -XX
PA (PERF.) PERCEPION PHARY INC

XX N vanconicular CP;
RT

XX WPB. 2000-293165/25
DB

XX	Related nucleic acid
PT	

to form a nonfunctional complex

Example 4; Fig 15; 152pp; English

The *inv* protein confers productivity of antagoconists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta receptor dimerization, the soluble alpha specificity determining component of the receptor (3R-alpha) and the extracellular domain of the first beta signal

sq Sequence 360 AA;

Query Match	100.0%	Score 105;	DB 21;	Length 360;
Best local Similarity	100.0%	Pred. No. 6,5e-09;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MCVASSNSSTFSTKTFQFQCC	20
Db	192	mcvassvskstsktcqtdgc	211

RESULT	12
AAP90526	
ID	AAP90526 standard; protein; 386 AA

DT 25-JAN-1990 (first entry)

DE B cell stimulating factor-2 receptor

KW B cell stimulating factor-2 receptor; monocyte U937 cell line.

OS Homo sapiens

PN AU8928720-A.

PD 27-JUL-1989

PF 23-JAN-1989; 89AU-0028720

PR 22-JAN-1988; 88JP-0012387

PR	04-AUG-1988;	88JP-0194885.
PR	14-JAN-1989.	89JP-0007461

XX
B3
KISHI \ TADAMITSU KISHIMOTO

XX
PT Kishimoto T.

WPT: 1989-264012/37

DK N-PSDB; AAAP;
XX

PT receptor protein ion developing probhla

PI ASSOCIATED ALSO
XX

CR 4; page 31-8; 1
PS
XX

The B22 receptor has residues-
is derived from a monocyte U937 cell

CC immunomechanism with which BSF-2 or the receptor is concerned.

SQ **Sequence** **386 AA**

Query Match	100.0%	Score 105; DB 10;	Length 386;
Best Local Similarity	100.0%	Pred. 6.9e-09;	
Matches 20; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0

RESULTS

ID	ANY30938	standard; Protein; 419 AA
XY		

XX

XX Receptor protein for human B cell stimulating factor-2 - obsd. by
 PF recombinant DNA techniques and used as diagnostic, prophylactic or
 PF therapeutic agent
 XX
 PS Claim 2: Page 19-21: 63pp: English.
 XX
 CC The cDNA in AAN90340 was derived from monocyte cell line U937.
 CC Isolated Bsf2 receptor and DNA encoding it are claimed, as are
 CC (b) expression vectors; (c) host organisms; (d) antibodies; and
 CC (e) hybridomas.
 XX

SO Sequence 468 AA:

Query Match 100.0%; Score 105; DB 10; Length 468;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCVASVSGSKFKTQFGCC 20
 |||||
 DB 192 MCVASVSGSKFKTQFGCC 211

Search completed: December 19, 2001, 16:19:35
 Job Time: 360 sec

F:387-468/Domain: Intracellular *status predicted <INT>
 F:151/468/Domain: Intracellular *status predicted <INT>
 F:353-93/221,245,350/Binding site: carbohydrate (asn) (covalent) *status predicted
 F:353-93/221,245,350/Binding site: carbohydrate (asn) (covalent) *status predicted

Query Match 100.0%; Score 105; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 20
 |||:|||||:|
 Db 192 MCVASSVSGSKFSKFTQFC 211

RESULT 2
 J10144
 Interleukin-6 receptor precursor (clone lambda p1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 *sequence_revision 31-Dec-1991 *text_change 21-Jan-2000
 C:Accession: J10144
 R:Singla, T.; Tachaka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A>Title: Functional murine Interleukin 6 receptor with the Intracisternal a particle get
 A:Reference number: J10144; MWID:90278354
 A:Accession: J10144
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: mRNA
 A:Residues: 1-440 <SNG>
 A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:119/Domain: signal sequence *status predicted <SIG>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane *status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 440;
 Best Local Similarity 38.8%; Pred. No. 0.53;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 17
 |||:|||||:|
 Db 189 LCVANVSGSKFSKSHNEAF 205

RESULT 3
 J10145
 Interleukin-6 receptor precursor (clone lambda 301) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 *sequence_revision 31-Dec-1991 *text_change 21-Jan-2000
 C:Accession: J10145; S14543
 R:Singla, T.; Tachaka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A>Title: Functional murine Interleukin 6 receptor with the Intracisternal a particle get
 A:Reference number: J10144; MWID:90278354
 A:Accession: J10145
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: mRNA
 A:Residues: 1-460 <SNG>
 A:Cross-references: GB:X51975; NID:949735; PIDN:CAA36237.1; PID:949736
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:119/Domain: signal sequence *status predicted <SIG>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane *status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 440;
 Best Local Similarity 38.8%; Pred. No. 0.53;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 17
 |||:|||||:|
 Db 189 LCVANVSGSKFSKSHNEAF 205

RESULT 4
 A37986
 Interleukin-6 receptor precursor - rat
 N:Alternate names: IL-6 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 22-Jun-1999
 C:Accession: A37986
 R:Singla, T.; Tachaka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A>Title: Functional murine Interleukin 6 receptor with the Intracisternal a particle get
 A:Reference number: J10144; MWID:90278354
 A:Accession: A37986
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: mRNA
 A:Residues: 1-462 <END>
 A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:119/Domain: signal sequence *status predicted <SIG>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane *status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 462;
 Best Local Similarity 38.8%; Pred. No. 0.53;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 18
 |||:|||||:|
 Db 189 LCVANVSGSKFSKSHNEAF 206

RESULT 5
 B71541
 Probable amino acid (glutamate) transporter - Chlamydia trachomatis (serotype D, str
 C:Species: Chlamydia trachomatis
 C:Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 18-Feb-2000
 C:Accession: B71541
 R:Singla, T.; Tachaka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A>Title: Functional murine Interleukin 6 receptor with the Intracisternal a particle get
 A:Reference number: J10144; MWID:90278354
 A:Accession: B71541
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: DNA
 A:Residues: 1-415 <ARN>
 A:Cross-references: GB:AE001296; GB:AE001273; NID:93328630; PIDN:MAC67822.1; PID:9332
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:119/Domain: signal sequence *status predicted <SIG>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane *status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 462;
 Best Local Similarity 38.8%; Pred. No. 0.53;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 18
 |||:|||||:|
 Db 189 LCVANVSGSKFSKSHNEAF 206

RESULT 5
 B71541
 Probable amino acid (glutamate) transporter - Chlamydia trachomatis (serotype D, str
 C:Species: Chlamydia trachomatis
 C:Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 18-Feb-2000
 C:Accession: B71541
 R:Singla, T.; Tachaka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A>Title: Functional murine Interleukin 6 receptor with the Intracisternal a particle get
 A:Reference number: J10144; MWID:90278354
 A:Accession: B71541
 A:Keywords: cytokine receptor; transmembrane protein
 A:Molecule type: DNA
 A:Residues: 1-415 <ARN>
 A:Cross-references: GB:AE001296; GB:AE001273; NID:93328630; PIDN:MAC67822.1; PID:9332
 C:Superfamily: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:119/Domain: signal sequence *status predicted <SIG>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:20-94/Product: Interleukin 6 receptor *status predicted <INT>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane *status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 462;
 Best Local Similarity 38.8%; Pred. No. 0.53;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 MCVASSVSGSKFSKFTQFC 18
 |||:|||||:|
 Db 189 LCVANVSGSKFSKSHNEAF 206

RESULT 11

hypothetical protein F27H5.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49226

R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.

submitted to the Protein Sequence Database, April 2000

A:Reference number: 225

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-687 <R>

A:Cross-references: EMBL:AL163852; GenBank:U000061; ATSP:F27H5.100

A:Experimental source: EMBL:ATSP:U000061; EMBL:U000061

A:Map position: 3

A:Introns: 76/73: 139/1: 197/2: 265/2: 366/2

C:Superfamily: Arabidopsis thaliana hypothetical protein F27H5.100

Query Match 41.0% Score 43: DB 2: Length 687:

Best Local Similarity 36.8% Pred. No. 28:

Matches 7: Conservative 6: Mismatches 0: Gaps 0:

1 MCYASVSGSKFSTOTPOG 19

446 ICIKSCGSEVRETTITG 464

RESULT 12

119X DNA helicase/primase-associated protein - equine herpesvirus 1 (strain AD4)

C:Species: equine herpesvirus 1

A:Note: host Equus caballus (domestic horse)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999

C:Accession: M36795 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999

R:Frederick, E.A.; R. A. M. S.; McBride, K.; Davison, A.J.

submitted to GenBank March 1992

A:Description: The DNA sequence of equine herpesvirus-1.

A:Reference number: A36805

A:Molecule type: DNA

A:Residues: 1-1081 <R>

A:Cross-references: GB:M36795; NID:933079; PIDN:A480242.1; PID:9330799

A:Experimental source: M.S.; McBride, K.; Davison, A.J.

A:Title: The DNA sequence of equine herpesvirus-1.

A:Reference number: A41831; MUID:9229556

A:Contents: annotation, possible protein-coding frames

A:Note: neither amino acid nor nucleotide sequence is given

C:Genetics:

A:Gene:

C:Superfamily: varicella-zoster virus gene 6 protein

Query Match 40.0% Score 42: DB 1: Length 1081:

Best Local Similarity 29.4% Pred. No. 66:

Matches 5: Conservative 10: Mismatches 2: Indels 0: Gaps 0:

1 MCYASVSGSKFSTOTP 17

423 VCIUAFISGVADKTY 439

RESULT 13

hypothetical protein SPAC29B12.07 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 25-Jan-1998 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38495

R:Gentles, S.; Church, C.M.; Barrell, B.G.; Rindram, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z21797

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1669 <R>

A:Cross-references: EMBL:Z29166; PIDN:CA1625.1; GenBank:U000066; SPDB:SPAC29B12.07

A:Experimental source: strain 972H7; cosmid c29B12

A:Gene: SPDB:SPAC29B12.07

A:Map position: 1

A:Introns: 664/2

Query Match 40.0% Score 42: DB 2: Length 1669:

Best Local Similarity 31.8% Pred. No. 12602:

Matches 9: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

3 VASVSGSKF 13

1525 VLSISGSKF 1535

RESULT 14

senenophosphate synthase - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 19-May-2000

C:Accession: A64054

R:Rietveld, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kitzman, E.F.; Kollavane

/ D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, D.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64054; MUID:95350630

A:Contents: nucleotide sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-323 <R>

A:Cross-references: GB:U3705; GB:I42023; NID:91573156; PIDN:AC21869.1; PID:91573160

C:Genetics:

A:Start codon: GTG

C:Superfamily: hydroxymethylase/formation protein hnp

C:Keywords: senenophosphate biosynthesis

Query Match 39.0% Score 41: DB 2: Length 323:

Best Local Similarity 53.8% Pred. No. 30:

Matches 7: Conservative 4: Mismatches 2: Indels 0: Gaps 0:

1 MCYASVSGSKF 13

182 MCKMISGSKF 194

RESULT 15

probable maturase cox11 - fission yeast (Schizosaccharomyces pombe) mitochondrion

C:Species: Schizosaccharomyces pombe

C:Date: 25-Jan-1998 #sequence_revision 20-Feb-1998 #text_change 24-Oct-2000

C:Accession: T38495

R:Gentles, S.; Church, C.M.; Barrell, B.G.; Rindram, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21797

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1669 <R>

A:Cross-references: EMBL:Z29166; PIDN:CA1625.1; GenBank:U000066; SPDB:SPAC29B12.07

A:Experimental source: strain 972H7; cosmid c29B12

A:Gene: SPDB:SPAC29B12.07

A:Map position: 1

A:Introns: 664/2

Query Match 40.0% Score 42: DB 2: Length 1669:

Best Local Similarity 31.8% Pred. No. 12602:

Matches 9: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

3 VASVSGSKF 13

1525 VLSISGSKF 1535

A:Experimental source: strain ad7-50h
 R:Scheetj, B.: Melios-Lange, A.M.: Anderl, C.: Welser, F.: Zimmer, M.: Wolf, K.
 A:Accession: S13339
 A:Reference number: S13339, MUID:91155928
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 132-152, 'L', 154-177, 'L', 179-186, 'L', 188-206, 'R', 208-262, 'T', 264-271, 'L', 273-
 7, 'T', 409-421, 'L', 424-429, 'L', 431-438, 'T', 440-448, 'T', 450-462, 'L', 464-494, 'L', 496-519
 A:Experimental source: mutant strain ana(gamma)-14
 A:Gene: coxII
 A:Genome: mitochondrion
 A:Genetic code: SGC2
 C:Superfamily: COI Intron 9 protein; COI Intron 9 protein homology
 C:Keywords: mitochondrion
 F:1-135/Region: coxI exon 1 encoded
 F:136-519/Region: coxI Intron encoded
 Query Match 39.0%; Score 41; DB 2; Length 519;
 Best Local Similarity 55.6%; Pred.No. 48;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 2 CVASSVGSFKFSKTQTFCG 19
 DB 231 CFSSSSPKFSPTQMLVQ 248

Search completed: December 19, 2001, 16:22:39
 Job time: 459 sec

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FT DISULFID 47 92 BY SIMILARITY.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 132 132 BY SIMILARITY.
 FT CARBOHYD 32 32 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CONFLICT 374 374 A -> R (IN REF. 2).
 SO SEQUENCE 460 AA: 50454 MW: P85C59D6D8525C4 CRC64:

Query Match 49.58: Score 52; DB 1; Length 460;
 Best Local Similarity 58.88; Pred. No. 0.16; Mismatches 4; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 189 LCYANVSWSKSSHNEAF 205

RESULT 4
 IL6A-RAT STANDARD: PRT: 462 AA.
 ID IL6A-RAT STANDARD: PRT: 462 AA.
 P22773.
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE INTERLEUKIN-6 (IL-6) (POTENTIAL).
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PROSEQUEN (IL-6R-ALPHA) (IL-6R.1).
 GN IL6R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RN SOURCE FROM N.A.
 RC STRAUB-FISCHER 344: TISSUE-Liver;
 RA Baumann M., Baumann H., Fey G.H.:
 RA "Molecular cloning, characterization and functional expression of the
 RA rat liver interleukin 6 receptor."
 RA J. Biol. Chem. 265:19853-19862(1990).
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
 RA Gibson T.:
 RA unpublished observations (FEB-1995).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION REQUIRES AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC BEOCCUR BY PHOSPHORYLATION OF IL6ST.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN-III-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF PROTEINS.
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 CC EMBL: M58587; AAA1431.1; -
 DR PIR: A37986; A37986.
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR001996; CRIA.
 DR InterPro: IPR001777; FN.ITI.
 DR InterPro: IPR001996; FN.ITI.
 DR InterPro: HEMATOPO_Topolo_L_F3.
 DR InterPro: IPR003066; 19_AHC.

DR InterPro: IPR003598; 19_C2.
 DR Pfam: PF00041; En3.1.
 DR SMART: SM00066; FN3.1.
 DR SMART: SM00408; ICG2.1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 462 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 20 385 POTENTIAL.
 FT TRANSMEM 365 385 POTENTIAL.
 FT DOMAIN 386 462 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 190 BY SIMILARITY.
 FT DISULFID 47 92 BY SIMILARITY.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 162 173 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CONFLICT 227 261 XPRALVSQDDPSMDPSVYDLPFLYPRWSKX
 FT CONFLICT 227 261 SILVSVSGVTLSPGQVYTCQSSPGYDILGORT
 FT CONFLICT 227 261 (IN REF. 1).
 SO SEQUENCE 462 AA: 50398 MW: A4B0D04CEBDC0537D CRC64:

Query Match 47.68: Score 50; DB 1; Length 462;
 Best Local Similarity 55.68; Pred. No. 0.4;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 189 LCYANVSWSKSSHNYEQ 206

RESULT 5
 IM08-ARATH STANDARD: PRT: 77 AA.
 ID IM08-ARATH STANDARD: PRT: 77 AA.
 Q9G6T4.
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8.
 GN TIM8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eudicotyledons; Eudicotyledons; Rosids; Rosales; Rosaceae; Rosaceae;
 CC NCBI_TaxID=3702.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bauer M.F., Brunner M., Hofmann S.:
 RA "Cloning and mapping of the TIM10/DOP gene family encoding small zinc
 RA finger proteins involved in mitochondrial carrier import."
 RA J. Biol. Chem. 274:16990-16995(1999).
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 CC EMBL: AF150083; AAD9990.1; -
 DR Transport: Protein transport; Translocation; Mitochondrion;
 KW Inner membrane.
 SO SEQUENCE 77 AA: 8750 MW: 47E5B41ED9D00E8F CRC64:

Query Match 41.98: Score 44; DB 1; Length 77;


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CC  or send an email to license@isb-sdb.ch).
CC  -----
CC  DR  EMBL: J12612; CAA73536.1; -.
CC  DR  MIM: 203920; -.
CC  KW  Nuclear protein; DNA-binding; SCID; Phosphorylation.
CC  FT  DOMAIN 38 41 POLY-ALA.
CC  FT  DOMAIN 171 178 POLY-ITS.
CC  FT  DOMAIN 163 178 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC  SQ  SEQUENCE 272 AA; 28232 MW; A675FE30D59F005 CRC64;
CC
QY  Query Match 41.0%; Score 43; DB 1; Length 272;
QY  Best local similarity 53.3%; Pred. No. 3;
QY  Matches 8; Conservative 2; Mismatches 5; Gaps 0;
QY  Db 132 SGGSGSNCTGTTC 146
QY
RESULT 9
ID  YP66_YEAST STANDARD; PRT; 479 AA.
AC  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  15-JUL-1998 (Rel. 37, Last annotation update)
DE  HYPOTHETICAL 54.9 KDA PROTEIN IN VP528-BTSL INTERGENIC REGION.
GN  YP1066W OR LPMW.
GS  Saccharomyces cerevisiae (Baker's Yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX  NCBI_TaxID=4932;
RX  NUCLEOTIDE SEQUENCE FROM N.A.
RA  Winnett E., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
RA  Stromberg R., Vo D.H., Wang Y.;
RA  Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL  This SWISS-PROT entry is copyright. It is produced through a collaboration
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RL  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
RL  or send an email to license@isb-sdb.ch).
CC  EMBL: U50630; -. NOT ANNOTATED COS.
CC  DR  EMBL: 300549; AB66229.1; -.
CC  DR  SDB: 000549; AB66229.1; -.
CC  KW  Hypothetical protein.
CC  SQ  SEQUENCE 479 AA; 54893 MW; DDC9FAA6AC6F74 CRC64;
CC
QY  Query Match 41.0%; Score 43; DB 1; Length 479;
QY  Best local similarity 72.7%; Pred. No. 6;
QY  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY  Db 139 KFKSTQTFDLC 149
QY
RESULT 10
ID  U152_HSVB STANDARD; PRT; 1081 AA.
AC  01-DEC-1992 (Rel. 24, Created)
DT  01-DEC-1992 (Rel. 24, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  DNA HELICASE/PRIMASE COMPLEX PROTEIN (DNA REPLICATION PROTEIN U152).
DE

```


KM Hypothetical protein: Mitochondrion.
 SQ SEQUENCE 384 AA; 45637 MW; C870AC922C78110D CMC64;
 Query Match 39.0%; Score 41; DB 1; Length 384;
 Best Local Similarity 55.6%; Pval. No. 12;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 OY 2 CAAAGSKFKSTQYFGC 19
 DB 96 CFASSSKFKSTQYFGC 113
 RESULT 13
 ID DSDS_NEIHA STANDARD; PRT; 601 AA.
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE THIO-DISULFIDE INTERCHANGE PROTEIN DSD PRECURSOR.
 OS DSD OR NHA1719.
 ON Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NM NCBI_TaxID=65859;
 [1]
 [2]
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KM Hypothetical protein: Mitochondrion.
 SQ SEQUENCE 384 AA; 45637 MW; C870AC922C78110D CMC64;
 Query Match 39.0%; Score 41; DB 1; Length 384;
 Best Local Similarity 55.6%; Pval. No. 12;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 OY 2 CAAAGSKFKSTQYFGC 19
 DB 96 CFASSSKFKSTQYFGC 113
 RESULT 13
 ID DSDS_NEIHA STANDARD; PRT; 601 AA.
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE THIO-DISULFIDE INTERCHANGE PROTEIN DSD PRECURSOR.
 OS DSD OR NHA1719.
 ON Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NM NCBI_TaxID=65859;
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RESULT 2
DB#433 PRELIMINARY: PRT: 415 AA.
AC 084233:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NEUTRAL AMINO ACID (GLUTAMATE) TRANSPORTER (GLUTAMATE).
GN CT330.
OS Chlamydia trachomatis.
NCBI_TaxID=811.
OX NCBI_TaxID=811.
RN SEQUENCE FROM N.A.
RP STRAIN=D/UM-1/3/CX; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Atavind L.,
RA Mitchell M.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RC "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
RA EMBL: AE001295; AAC67822.1.
DR InterPro: IPR001991; Ne_dclarboxyl_symp.
DR Pfam: PF00375; SDF: 1.
RN SEQUENCE PROTOCOL:
SO SEQUENCE 415 AA; 4506 MW; 627AF6718FB74 CRC64;

Query Match 43.8%; Score 46; DB 2; Length 415;
Best Local Similarity 42.1%; Pred. No. 7.1;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

2 CVAASVSGSKRTQFGC 20
DB 392 CVAASVSKREFEDLPFC 410
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RESULT 3
DB#433 PRELIMINARY: PRT: 687 AA.
AC 091X34:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HYPOTHETICAL 76.5 KDA PROTEIN.
GN F27B_100.
OS Arabidopsis thaliana (Mouse-ear cress).
NCBI_TaxID=10116.
OX NCBI_TaxID=10116.
RN SEQUENCE FROM N.A.
RP Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.N., Rüd S.,
RA Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RA Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RA EMBL: AL163852; CAB87868.1.
DR InterPro: IPR01919; CYLD_b6.
DR Pfam: PF00493; MYOCHROME_D_OO; UNKNOWN_1.
RN Hypothetical protein.
SO SEQUENCE 687 AA; 76489 MW; 61BB48896620F17 CRC64;

Query Match 41.0%; Score 43; DB 10; Length 687;
Best Local Similarity 36.8%; Pred. No. 39;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 MCVAASVSGSKRTQFG 19

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DB#446 ICISGSGSENVETITG 464
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RESULT 4
DB#446 PRELIMINARY: PRT: 688 AA.
AC 09GNP2:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE VASA HOMOLOG.
GN CSEADIA(CSVH).
OS Ciona savignyi.
NCBI_TaxID=51511.
OX NCBI_TaxID=51511.
RN SEQUENCE FROM N.A.
RP TISSUE-OVARY:
RA MEDLINE=20130953; PubMed=10664149;
RA Fujimura M., Takamura K.;
RC "Characterization of an ascidian DEAD-box gene, C1-DEAD1: specific
RT expression in the germ cells and its mRNA localization in the
RT posterior-most blastomeres in early embryos."
BL Science 291:615-620(2000)
CC -1- SIMILARITY: BELONGS TO 2N-FINGER CCHC TYPE FAMILY.
CC -1- SIMILARITY: TO DEAD/DEAF BOX HELICASE FAMILY.
CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
DR EMBL: AB047802; BAB1216.1.
DR InterPro: IPR01410; DEAD.
DR InterPro: IPR01878; HELICASE_C.
DR Pfam: PF00270; DEAD_1; HELIC.
DR Pfam: PF00271; Helicase_C.1.
DR Pfam: PF00398; zf-CCHC; 3.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICG; 1.
DR SMART: SM00343; ZNF-C2HC; 3.
RN SEQUENCE FROM N.A.
SO SEQUENCE 688 AA; 73744 MW; 7AE20CF80AA681B9 CRC64;

Query Match 41.0%; Score 43; DB 5; Length 688;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

2 CVAASVSGSKRTQFG 19
DB 619 CVAASVSGSKRTQFGS 636
|||||:|||||

RESULT 5
DB#446 PRELIMINARY: PRT: 770 AA.
AC 09GNP1:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE VASA HOMOLOG.
GN CSEADIB(CSVH).
OS Ciona savignyi.
NCBI_TaxID=51511.
OX NCBI_TaxID=51511.
RN SEQUENCE FROM N.A.
RP TISSUE-OVARY:
RC MEDLINE=20130953; PubMed=10664149;
RA Fujimura M., Takamura K.;
RC "Characterization of an ascidian DEAD-box gene, C1-DEAD1: specific
RT expression in the germ cells and its mRNA localization in the
RT posterior-most blastomeres in early embryos."

```

Query Match 100.0%; Score 105; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 80 MCVASSVSGSKFSKFTQFGC 99

RESULT 3
5171840-6
Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
FILING DATE: 02-JUL-1992
PRIORITY APPLICATION NUMBER: 05/07/298,694
SEQ ID NO:6:
LENGTH: 323
5171840-6

Query Match 100.0%; Score 105; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 192 MCVASSVSGSKFSKFTQFGC 211

RESULT 4
5480796-6
Patent No. 5480796
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: 02-JUL-1992
PRIORITY APPLICATION NUMBER: 298,694
SEQ ID NO:6:
LENGTH: 323
5480796-6

Query Match 100.0%; Score 105; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 192 MCVASSVSGSKFSKFTQFGC 211

RESULT 5
5171840-7
Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
FILING DATE: 05/07/298,694
SEQ ID NO:7:
LENGTH: 344

5171840-7
Query Match 100.0%; Score 105; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 192 MCVASSVSGSKFSKFTQFGC 211

RESULT 6
5480796-7
Patent No. 5480796
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: 02-JUL-1992
PRIORITY APPLICATION NUMBER: 298,694
SEQ ID NO:7:
LENGTH: 344
5480796-7

Query Match 100.0%; Score 105; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 192 MCVASSVSGSKFSKFTQFGC 211

RESULT 7
5171840-5
Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
FILING DATE: 05/07/298,694
SEQ ID NO:5:
LENGTH: 386
5171840-5

Query Match 100.0%; Score 105; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MCVASSVSGSKFSKFTQFGC 20
|||||
Db 110 MCVASSVSGSKFSKFTQFGC 129

RESULT 8
5480796-5
Patent No. 5480796
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: 02-JUL-1992

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5
; LENGTH: 386
5480796-5

```

```

Query Match      Score 105; DB 6; Length 386;
Best local similarity 100.0%; Pred. No. 48-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07      1 MCYASVGSKSKSTQTFQGC 20
      |||.....
Db      110 MCYASVGSKSKSTQTFQGC 129

```

```

1      RESULT 9
2      / Sequence 5, Application US/08/95473B
3      / Patent No. 6,217,853
4      / GENETIC INFORMATION:
5      / APPLICANT: Galun, Eitan
6      / APPLICANT: Nahot, Ofir
7      / APPLICANT: Blum, Herbert A.
8      / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
9      / TITLE OF INVENTION: Herpes B Virus (HBV) Infection
10     / NUMBER OF SEQUENCES: 10
11     / CORRESPONDENCE ADDRESS:
12     / ADDRESSEE: Davidson, Davidson and Kappel, LLC
13     / STREET: 1140 Avenue of the Americas
14     / SUITE: 4000
15     / STATE: New York
16     / COUNTRY: USA
17     / ZIP: 10036
18     / COMPUTER READABLE FORM:
19     / MEDIUM TYPE: 3.5 Inch disk
20     / COMPUTER: IBM PC compatible
21     / OPERATING SYSTEM: PC-DOS/MS-DOS
22     / SOFTWARE: MS-DOS Editor
23     / CURRENT APPLICATION DATA:
24     / FILING DATE: 11-FEB-1997
25     / CLASSIFICATION:
26     / ATTORNEY/AGENT INFORMATION:
27     / NAME: Davidson, Clifford M.
28     / REGISTRATION NUMBER: 32,728
29     / REFERENCE/DOCKET NUMBER: 963,1007
30     / TELEPHONE: (212) 991,0128
31     / TELEPHONE: (212) 969,10128
32     / INFORMATION FOR SEQ ID NO: 5:
33     / SEQUENCE CHARACTERISTICS:
34     / LENGTH: 468 amino acids
35     / TYPE: amino acid
36     / TOPOLOGY: unknown
37     / IS-08-795-473B-5

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Query Match 100.0%; Score 105; DB 4; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4, 9e-09;
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Dy 1 MCASVSGSRFSKTPFGGC 20
 |||
 Db 192 MCVASSVGSFRKTPFGGC 211

RESULT 10
 517840-2
 : Patent No. 517840
 : APPLICANT: KISHIMOTO, TADAMITSU
 : TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

```

:STIMULATORY FACTOR-2
:
:NUMBER OF SEQUENCES: 11
:
:CURRENT APPLICATION DATA:
:APPLICATION NUMBER: US/07/298,694
:
:FILING DATE: 19-JAN-1989
:
:SEQ ID NO:2
:
:LENGTH: 468
517840-2

```

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Query Match          100.0%; Score 105; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 4,9e-09;
Matches    20; Conservative   0; Mismatches    0; Indels      0; Gaps      0;
```

RESULT 11
 5480796-2
 Patent No. 5480796
 INVENTOR: KAZUHIRO, TADANISU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/07/907,650
 FILING DATE: 02-JUL-1992
 PRIORITY DATE: 02-JUL-1992
 APPLICATION NUMBER: 598,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO.: 2
 LENGTH: 468
 5480796-2

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Query Match      100.0% Score 105; DB 6; Length 468;
Best local similarity 100.0%; Pval. No. 4-9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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RESULT 12
 US-07-929-5608-5
 Sequence 5, Application US/07929580B
 Patent No. 5426181
 INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Lee, Gene W.
 APPLICANT: Altsch, Jan
 TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
 TITLE OF INVENTION: DNA Coding Thereof and Uses Thereof
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech and Nektar
 460 Point San Bruno Avenue
 City: Washington
 STATE: DC
 COUNTRY: US
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: S-DOS
 SOFTWARE: Patentin Release #124
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/929,580B
 FILING DATE: 19920814
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/640,492
 INVENTOR: LILLY, JAMES H.
 ATTORNEY/AGENT INFORMATION:
 NAME: TOMSSEND, GUY KEVIN
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: LEE25\VLICKER-2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 757-3528
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS: 3;
 LENGTH: 201 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-929-5608-5

Query Match 37.1%; Score 39; DB 1; Length 201;
 Best Local Similarity 50.0%; Pred. No. 55;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 SVGSRSKRTQPG 19
 DB 116 SYGGRDRSGSYVG 149

RESULT 13

US-07-708-8658-3
 Sequence 3, Application US/077088658

GENERAL INFORMATION:
 APPLICANT: Maswowe, Sibusiswe M.

APPLICANT: Brigman, Joseph V.

APPLICANT: Toth, Carol A.

TITLE OF INVENTION: Method for Isolating

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Disette, 3.5 inch, 720kb storage

OPERATING SYSTEM: DOS 3.30

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/708,8658

FILING DATE: 19910531

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 223 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

NAME/KEY: C-reactive protein

PUBLICATION INFORMATION:

AUTHORS: Lei, Ke-jian

AUTHORS: Liu, Teresa

AUTHORS: Zou, Gerald

AUTHORS: Sotavila, Emilia

AUTHORS: Liu, Teh-Yung
 TITLE: Genomic Sequence for Human
 JOURNAL: J of Biological Chemistry
 VOLUME: 260
 ISSUE: 24
 PAGES: 13377-83
 DATE: 25 Oct 1985
 US-07-708-8658-3

Query Match 37.1%; Score 39; DB 1; Length 223;
 Best Local Similarity 50.0%; Pred. No. 62;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 SVGSRSKRTQPG 19
 DB 158 SYGGRDRSGSYVG 171

RESULT 14

US-07-714-386-3
 Sequence 3, Application US/07714386

PATENT No. 5278290

GENERAL INFORMATION:

APPLICANT: Toth, Carol A.

APPLICANT: Maswowe, Sibusiswe M.

APPLICANT: Brigman, Joseph V.

TITLE OF INVENTION: Binding Protein for

TITLE OF INVENTION: CEA and Uses Thereof

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Disette, 3.5 inch, 720kb storage

OPERATING SYSTEM: DOS 3.30

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/714,386

FILING DATE: 19910531

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 223 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

NAME/KEY: C-reactive protein

PUBLICATION INFORMATION:

AUTHORS: Lei, Ke-jian

AUTHORS: Liu, Teresa

AUTHORS: Zou, Gerald

AUTHORS: Sotavila, Emilia

AUTHORS: Goldman, Neil D.

TITLE: Genomic Sequence for Human

JOURNAL: J. of Biological Chemistry

VOLUME: 260

ISSUE: 24

PAGES: 13377-83

Copyright (c) 1993 - 2000 CompuGen Ltd.

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:35 ; Search time 170.68 Seconds

(without alignments)

Title: US-09-202-104a-7

Sequence: 1 PEKPKMLSTGNEKRRKRDGGR 25

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

522463 seqs, 7407390 residues

Searched: 522463

Total number of hits satisfying chosen parameters:

522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Maximum Match 0%

Post-processing: Minimum Match 0%

Database:

Listing first 45 summaries

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22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	25	19	AAW52207
2	145	100.0	180	17	AAW00404
3	145	100.0	329	18	AAW17859
4	145	100.0	332	21	AAW01759
5	145	100.0	656	17	AAW94576
6	145	100.0	708	14	AAW17804
7	145	100.0	708	17	AAW85911
8	145	100.0	727	21	AAW92192
9	145	100.0	738	21	AAW92193
10	145	100.0	859	20	AAW70796

12	145	100.0	859	21	AAW92184	Human gp130-Fc-His
13	145	100.0	918	12	AAW10545	Recombinant human
14	145	100.0	918	15	AAW46233	Human soluble glyco
15	145	100.0	918	17	AAW75368	Human gp130 protein
16	145	100.0	925	20	AAW107928	Human gp130 protein
17	145	100.0	951	21	AAW92186	Human gp130-C-gamm
18	145	100.0	951	21	AAW92187	Human gp130-C-gamm
19	145	100.0	951	21	AAW92188	Human gp130-C-gamm
20	145	100.0	1158	21	AAW92205	Fusion polypeptide
21	145	100.0	1158	21	AAW92206	Fusion polypeptide
22	116	80.0	24	22	AAW88320	Human Interleukin-
23	110	75.9	917	13	AAW28334	Human gp130-Fc-His
24	110	75.9	917	13	AAW28335	Human gp130-Fc-His
25	110	75.9	917	13	AAW28336	Human gp130-Fc-His
26	79	54.5	13	22	AAW48708	Human IL-6 receptor
27	67	46.2	252	22	AAW51243	Human haemopoietin
28	67	46.2	652	22	AAW51242	Human haemopoietin
29	67	46.2	662	22	AAW51244	Human haemopoietin
30	65.5	45.2	862	18	AAW12771	Human Interleukin-
31	64	44.1	13	22	AAW48709	Human IL-6 receptor
32	63	43.4	303	20	AAW70843	Human Zcyto5 vari
33	63	43.4	303	20	AAW70845	Human Zcyto5 vari
34	63	43.4	350	19	AAW55015	Human Zcyto5 vari
35	63	43.4	350	22	AAW08824	Human N66 haemopo
36	63	43.4	385	20	AAW70842	Human Zcyto5 vari
37	63	43.4	388	20	AAW70839	Human Zcyto5 vari
38	63	43.4	389	20	AAW70840	Human Zcyto5 vari
39	63	43.4	389	20	AAW70841	Human Zcyto5 vari
40	63	43.4	389	20	AAW70842	Human Zcyto5 vari
41	63	43.4	389	20	AAW70843	Human Zcyto5 vari
42	63	43.4	389	20	AAW70844	Human Zcyto5 vari
43	63	43.4	389	20	AAW70845	Human Zcyto5 vari
44	63	43.4	389	20	AAW70851	Human Zcyto5 vari
45	63	43.4	389	20	AAW70852	Human Zcyto5 vari

ALIGNMENTS

RESULT	1
AAW52207	standard: peptide: 25 AA.
XX	AAW52207:
XX	09-JUN-1998 (first entry)
XX	Interleukin-6 antagonist peptide.
XX	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW	acquired immune deficiency syndrome-related lymphoma; immune response;
KW	hematological disorders; psoriasis; sepsis; osteoporosis; therapy;
KW	Alzheimer's disease.
XX	Synthetic.
OS	Human sapiens.
XX	MO9748728-A1.
XX	24-DEC-1997.
XX	19-JUN-1997: 97MO-RL00345.
XX	20-JUN-1996: 96EP-0201720.
XX	(KOSTY) KOSTER H W.
XX	Hoebe KHN, Van Leengoed LMG;
XX	WPI: 1998-063080/06.
DR	New peptide(s) with interleukin-6 agonist or antagonist activity -
PT	useful for treatment, prevention and diagnosis of IL-6 associated

PF diseases
 XX
 XX
 XX Claim 6, page 17; 28pp; English.
 CC This sequence represents a Interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC examples include multiple myeloma, acquired immune deficiency
 CC syndrome, and Alzheimer's disease etc.); also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects; also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC immunogenic). They may be used in combination with other drugs, e.g.,
 CC hepatocyte(s), have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 XX
 XX Sequence 25 AA:
 SO
 Query Match 100.0%; Score 145; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6,4e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PEKRNLSCTVNEGKKKRCNDGSR 25
 1 pdkpnlsvetneqkkrncdgsgr 25
 Db 1 pdkpnlsvetneqkkrncdgsgr 25
 RESULT 2
 AAM00404 standard; peptide: 180 AA.
 ID AAM00404;
 XX
 XX AAM00404;
 DT 29-AUG-1996 (first entry)
 DE Interleukin-6 antagonist peptide.
 XX
 XX IL-6; antagonist; autoimmune disease.
 XX
 XX Synthetic.
 XX
 XX JF07324097-A.
 XX
 XX 12-DEC-1995.
 PD
 XX 30-MAY-1994; 94JP-0117259.
 PR
 XX 30-MAY-1994; 94JP-0117259.
 PR
 XX (DAIICEL CHEM IND LTD.
 PA (FUJII) FUJISAWA PHARM CO LTD.
 XX
 XX WPI; 1996-065476/07.
 DB
 XX
 XX Interleukin 6 antagonist - useful for treating auto-immune diseases
 XX
 XX Claim 1; Page 2; 19pp; Japanese.
 PS
 XX
 XX New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAM00404, AAM00405, AAM00403 or AAM00404 (the
 CC present sequence), where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from
 CC the present sequence (AAM00436 - AAM00442) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 XX
 XX Sequence 180 AA:
 SO
 Query Match 100.0%; Score 145; DB 17; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5,2e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PEKPNLSCTVNEGKKKRCNDGSR 25
 4 pdkpnlsvetneqkkrncdgsgr 28
 Db 4 pdkpnlsvetneqkkrncdgsgr 28
 RESULT 3
 AAM17859 standard; Protein: 329 AA.
 ID AAM17859
 AC AAM17859;
 XX
 XX 04-FEB-1998 (first entry)
 DT
 XX
 XX Rheumatoid arthritis auto-antigen clone A.
 XX
 XX Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
 XX prediction; synovial cell.
 XX
 XX Homo sapiens.
 OS
 XX M09717441-A1.
 PM
 XX
 XX 15-MAY-1997.
 PR
 XX
 XX 06-NOV-1996; 96WO-JP03250.
 PE
 XX
 XX 07-NOV-1995; 95JP-0288957.
 PR
 XX
 XX (KANF) KANEKA CORP.
 XX
 XX Kishimura M, Nakao K, Oshikado F, Osaka S, Tanaka M;
 XX
 XX WPI: 1997-281030/25.
 DB
 XX
 XX N-PSDB: AAT68830.
 PF
 XX
 XX Auto-antigen from synovial cells of rheumatoid arthritis patients -
 CC binds to antibodies present in these patients, for diagnosis and
 CC prediction of the disease
 XX
 XX Claim 3; Pages 36-37; 61pp; Japanese.
 PS
 XX
 XX The present sequence is the Rheumatoid arthritis (RA) auto-antigen
 CC clone A, which can be used to diagnose and predict the development
 CC of RA by reaction with antibodies in biological specimens, e.g.
 CC sera, isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using 19C separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression
 CC vector for the transformation of E. coli NM522. Transformants on
 CC culture express clone A peptide and folistatin related protein
 CC into the culture medium.
 XX
 XX Sequence 329 AA:
 SO
 Query Match 100.0%; Score 145; DB 18; Length 329;
 Best Local Similarity 100.0%; Pred. No. 9,9e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PEKRNLSCTVNEGKKKRCNDGSR 25

AA85911 standard; Protein: 708 AA.
 AA85911:
 03-JUL-1996 (first entry)
 gp130 N-terminal fragment.
 Human: gp130; inhibitor: oncostatin M; cytokine; antibody Fc region;
 oncostatin M receptor-beta chain; antibody; tumour; growth factor;
 therapy.
 Homo sapiens.
 Key
 Peptide
 Location/Qualifiers
 1..22
 /note="signal peptide"
 23..708
 /note="N-terminal fragment of mature gp130"
 Modified-site
 21..23
 /note="glycosylation site"
 Modified-site
 61..63
 /note="glycosylation site"
 Modified-site
 109..111
 /note="glycosylation site"
 Modified-site
 135..137
 /note="glycosylation site"
 Cleavage-site
 133..134
 /note="glycosylation site"
 Modified-site
 135..136
 /note="glycosylation site"
 Modified-site
 224..226
 /note="glycosylation site"
 Modified-site
 357..359
 /note="glycosylation site"
 Modified-site
 361..363
 /note="glycosylation site"
 Modified-site
 368..370
 /note="glycosylation site"
 Modified-site
 531..533
 /note="glycosylation site"
 Modified-site
 542..544
 /note="glycosylation site"
 Cleavage-site
 621..622
 /note="glycosylation site"
 WO9533059-A2.
 07-DEC-1995.
 22-MAY-1995; 95NO-US06530.
 12-SEP-1994; 94US-030881.
 26-MAY-1994; 94US-0249553.
 (TMMV) IMMUNEX CORP.
 Cosman DJ, Mosley B;
 WPI: 1996-030570/03.
 N-PSDB: AA074081.
 Hetero-dimeric receptor proteins comprising OSW-R beta and gp 130 -
 bind oncostatin M and are used in inhibiting biological activities
 mediated by oncostatin M
 Claim 1: Page 35-38; 60pp; English.
 This sequence represents an N-terminal fragment of gp130 obtained from
 human placenta. gp130 binds to oncostatin M, which is a secreted single
 chain protein. The gp130 protein is a heterodimeric receptor protein,
 certain thereof derived and normal cell lines. This sequence can be
 the oncostatin M receptor-beta chain (see AA85912) sequence can be
 covalently joined, to give a heterodimeric receptor protein capable of
 binding to oncostatin M. The receptors can also comprise fusion

polypeptides, where an antibody Fc region is joined to the C-terminus of
 each of the soluble proteins. In this case, the two fusion polypeptides
 are joined by disulphide bonds between the two antibody Fc regions. The
 heterodimeric receptors can be used to inhibit biological activities
 mediated by oncostatin M. The advantage with using the heterodimeric
 receptors is that they bind to oncostatin M at greater levels than gp130
 does alone.
 Sequence 708 AA:
 Query Match 100.0%; Score 145; DB 17; Length 708;
 Best Local Similarity 100.0%; Pct. Id 2.2e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PERKRLSCTVNEGRKNCRCMDGGR 25
 Db 126 PEKRLSCTVNEGRKNCRCMDGGR 150
 RESUW 9
 AA92192
 ID AA92192 standard; protein: 727 AA.
 XX
 AC AA92192:
 DT 01-AUG-2000 (first entry)
 XX
 XX human gp130-kappa domain fusion protein.
 DE
 KW gp130-kappa domain; cytokine; antagonist; CNRP; receptor; fusion protein;
 KW cytosolic; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key
 XX Protein
 FT 1 619
 FT /label="gp130
 FT Peptide
 FT 620..621
 FT /note="Ser-gly bridge"
 FT Protein
 FT 622..727
 FT /label="IgG1-kappa_domain
 XX
 XX WO200018932-A2.
 XX
 XX 06-APR-2000.
 XX
 XX 22-SEP-1995; 95NO-US22045.
 XX
 XX 25-SEP-1996; 95US-0101858.
 PR 19-MAY-1995; 95US-0131942.
 XX
 XX (RESE-) REGENERON PHARM INC.
 XX
 XX Stahl N, Yancopoulos GD;
 PI
 XX
 DR WPI: 2000-293165/25.
 XX
 XX Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 PT
 XX Example 4: Page 7; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a nonfunctional complex.
 CC The invention also provides a method for inhibiting the biological activity
 CC of a signal transducing component causing beta-receptor dimerization. The
 CC soluble alpha specifically determining component of the receptor
 CC (R-1) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to

CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CMF (cellary
 CC factor) and the IL-6 receptor. The IL-6 receptor is a heterodimer
 CC consisting of a ligand, a non-functional intermediate complex, and
 CC the presence of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed. It will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CMF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining 30
 CC amino acids. The extracellular domain of the alpha specifically determining
 CC the cytokine inaccessibility to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia. The gp130 and kappa domain
 CC sequence given in figures 9 and 13 of the specification.

Sequence 727 AA:

Query Match 100.0%: Score 145; DB 21; Length 727;

Best Local Similarity 100.0%: Pred. No. 2,3e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 126 pekpknlscivngkkmckmcdggr 150

RESULT 10

AAV92194 standard; protein; 738 AA.

AAV92194;

01-AUG-2000 (first entry)

Human gp130-J-kappa fusion protein.

gp130-J-kappa: cytokine; antagonist; CMF; receptor; fusion protein;

Synthetic.

Homo sapiens.

Key

Protein

Peptide

Peptide

Domain

Domain

Domain

Domain

Domain

Domain

Domain

Domain

Domain

PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex.
 XX Example 4: Page 7, 152pp: English.

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC component, can be formed. It will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CMF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining 30
 CC amino acids. The extracellular domain of the alpha specifically determining
 CC the cytokine inaccessibility to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

Sequence 738 AA:

Query Match 100.0%: Score 145; DB 21; Length 738;

Best Local Similarity 100.0%: Pred. No. 2,4e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 126 pekpknlscivngkkmckmcdggr 150

RESULT 11

AAW70796 standard; protein; 859 AA.

AAW70796;

03-FEB-1999 (first entry)

Human gp130-Fe-His6 amino acid sequence.

gp130: cytokine antagonist; interleukin; gamma-interferon;

granulocyte macrophage colony-stimulating factor; J peptide;

transforming growth factor-beta.

Synthetic.

Homo sapiens.

Key

Protein

Peptide

Peptide

Peptide

Peptide

AA10545
 AA10545 standard. Protein: 918 AA.
 AC
 AA10545:
 DT 12-APR-1991 (first entry)
 DE Recombinant human gp130 protein.
 DE Recombinant human gp130. Interleukin-6. Interleukin-6 receptor:
 CC Immunology; hematopoiesis; inflammation; therapy.
 CC Homo sapiens.
 XX
 XX EP11946-A.
 XX 06-FEB-1991.
 XX
 XX 02-AUG-1990: 90EP-0308530.
 XX
 XX 31-MAY-1990: 90UP-0140069.
 XX 03-AUG-1989: 89JP-0200230.
 XX
 XX (KISHI/) KISHIMOTO T.
 XX
 XX Kishimoto T.
 XX
 XX WPI: 1991-038820/06.
 XX N-PSDB: AAQ10402.
 DR
 XX
 XX Recombinant human gp130 protein - acts in the transmission of
 PT Interleukin-6 signal for defence mechanisms
 CC
 XX Disclosure: fig 7, 32pp; English.
 CC
 CC This gp130 protein is produced using standard recombinant DNA
 CC methods (see AAQ10402), free from any other human protein. It
 CC participates in the transmission of the interleukin (IL)-6 sig-
 CC nal, and therefore the proliferation and differentiation of an
 CC organism. It is important in an animals defence mechanisms, e.g.
 CC immunity, hematopoiesis and inflammation.
 CC
 XX
 XX Sequence 918 AA:
 SO
 Query Match 100.0%; Score 145; DB 12; Length 918;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PERKRNICTYNEGKKRRCEDGGR 25
 DB 126 pekphnlsctyngkkrccwdggr 150
 RESULT 14
 AAR46233
 AAR46233 standard. Protein: 918 AA.
 AC
 AAR46233:
 DT 15-SEP-1994 (first entry)
 DE Human soluble glycoprotein (gp) 130.
 DE
 CC Glycoprotein; soluble; gp; gp130; antibody production; assay;
 CC immunochimical assay; detection; immunogen; transmembrane domain.
 CC Homo sapiens.
 XX
 XX JF06022786-A.
 XX 01-FEB-1994.
 XX
 XX

EF 02-AUG-1991: 91JP-0217924.
 XX
 XX 02-AUG-1991: 91JP-0217924.
 XX
 XX (KISHI/) KISHIMOTO C.
 XX (TOYU) TOSOH CORP.
 XX
 XX WPI: 1994-071006/09.
 XX N-PSDB: AAQ565931.
 DR
 XX Preparation of recombinant soluble human gp 130 deriv - for use
 PT in the production of anti-gp 130 antibody for immunochemical
 PT assay
 CC
 XX Claim 1: Figure 7, 13pp; Japanese.
 XX
 XX The soluble glycoprotein (gp) 130 can be used as an immunogen for
 CC the preparation of anti-gp130 antibody and as the standard substance
 CC for immunochemical assay of gp130. Soluble gp130 cDNA was prepared
 CC by inserting a termination codon prior to the extracellular domain
 CC or transmembrane domain of the gp130 coding sequence or simply by
 CC eliminating the transmembrane domain.
 CC
 XX
 XX Sequence 918 AA:
 SO
 Query Match 100.0%; Score 145; DB 15; Length 918;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PERKRNICTYNEGKKRRCEDGGR 25
 DB 126 pekphnlsctyngkkrccwdggr 150
 RESULT 15
 AAR75368
 AAR75368 standard. Protein: 918 AA.
 AC
 AAR75368:
 DT 20-JUN-1996 (first entry)
 DE Human gp130 protein.
 DE
 CC Gp130; transmembrane domain; growth factor antagonist;
 CC embryo pre-implantation; in vitro fertilisation.
 CC
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 620..641
 FT /label= Transmembrane_region
 XX
 XX MO9609382-A1.
 XX
 XX 28-MAR-1996.
 XX
 XX 21-SEP-1995: 95MO-C802243.
 XX
 XX 21-SEP-1994: 94GB-0019021.
 XX
 XX (ISTF) ARS APPLIED RES SYST HOLDING NV.
 XX
 XX Dellow KA, Sharkey A, Smith SK:
 XX WPI: 1996-188444/19.
 XX N-PSDB: AAT14603.
 DR
 XX New splice variant of gp130 lacking the trans-membrane domain
 PT useful as an antagonist for growth factors esp. for ensuring correct
 PT development of pre-implantation embryos
 PT
 XX

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A:Experimental source: strain Wistar
C:Genetics:
A:Note: PTPRO
C:Key words: phosphoric monoester hydrolase
F:19-2302/Status: predicted <sig>
F:19-2302/Product: protein tyrosine phosphatase receptor type, GM1 #status predicted <sig>
Query Match 33.8%; Score 49; DB 2; Length 2302;
Best Local Similarity 28.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
Q7 1 PERKINSCITNECKKRCRRCGR 25
1343 PEAVRNIECVAROMQSVSRMDPPR 1367
DB 1343 PEAVRNIECVAROMQSVSRMDPPR 1367
Search completed: December 19, 2001, 16:22:39
Job time: 459 sec

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CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC -1- DISASE: gp130-RADS IS AN ANOMALOUS ROUND IN HEMATOPOIETIC
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD130 entry:
 CC NAME-http://www.ncbi.nlm.nih.gov/row/cd/cd130.htm
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 CC EMBL: M57230: AA59155.1: -
 CC EMBL: AB015706: BA078112.1: -
 CC PIR: A36337: A36337.
 CC PIR: 1BQ0: 26-AUG-98.
 CC MIR: 600594: -
 CC InterPro: IPR002996: CRIA.
 CC InterPro: IPR01777: FN.III.
 CC Pfam: PF00041: fn3.3
 CC Pfam: PF00014: PNTYPE.III.
 CC SMART: SM00060: FN3.3.
 CC PROSITE: PS01353: HEMATOPOIETIC L-F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat: 3D-structure; Alternative splicing.
 CC CHAIN: 1 918
 CC DOMAIN: 21 619
 CC TRANSMEM: 620 641
 CC DOMAIN: 642 918
 CC DOMAIN: 26 120
 CC DOMAIN: 124 222
 CC DOMAIN: 223 424
 CC DOMAIN: 424 517
 CC DOMAIN: 518 613
 CC DOMAIN: 725 755
 CC DISULFID: 28 54
 CC DISULFID: 148 103
 CC DISULFID: 134 144
 CC DISULFID: 452 462
 CC CARBOHYD: 43 43
 CC CARBOHYD: 83 83
 CC CARBOHYD: 131 131
 CC CARBOHYD: 157 157
 CC CARBOHYD: 227 227
 CC CARBOHYD: 329 329
 CC CARBOHYD: 353 353
 CC CARBOHYD: 553 553
 CC CARBOHYD: 554 554
 CC VARSPLIC: 335 329
 CC VARSPLIC: 330 918
 CC SEQUENCE 918 AA: 103522 MW: DB13F36720D10D53 CRC64:
 Query Match 100.0%: Score 145. DB 1: Length 918;
 Best Local Similarity 100.0%: Pident 4,7e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

IL56_MOUSE STANDARD: Ref: 917 AA.
 CC -1- DISASE: gp130-RADS IS AN ANOMALOUS ROUND IN HEMATOPOIETIC
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD130 entry:
 CC NAME-http://www.ncbi.nlm.nih.gov/row/cd/cd130.htm
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 CC EMBL: M57230: AA59155.1: -
 CC EMBL: AB015706: BA078112.1: -
 CC PIR: A36337: A36337.
 CC PIR: 1BQ0: 26-AUG-98.
 CC MIR: 600594: -
 CC InterPro: IPR002996: CRIA.
 CC InterPro: IPR01777: FN.III.
 CC Pfam: PF00041: fn3.3
 CC Pfam: PF00014: PNTYPE.III.
 CC SMART: SM00060: FN3.3.
 CC PROSITE: PS01353: HEMATOPOIETIC L-F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat: 3D-structure; Alternative splicing.
 CC CHAIN: 1 917
 CC DOMAIN: 21 619
 CC TRANSMEM: 618 639
 CC DOMAIN: 640 917
 CC DOMAIN: 26 120
 CC DOMAIN: 124 220
 CC DOMAIN: 221 322
 CC DOMAIN: 323 420
 CC DOMAIN: 422 515
 CC DOMAIN: 516 611
 CC DOMAIN: 723 741
 CC SEQUENCE 917 AA: 103521 MW: DB13F36720D10D53 CRC64:
 Query Match 100.0%: Score 145. DB 1: Length 917;
 Best Local Similarity 100.0%: Pident 4,7e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
 CC IL12RB2.
 CC -1- SUPRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC
 CC EMBL: U64198; AA33675.1;
 CC HSP: P40189; IBOU.
 CC Interpro: IPR001777; FN.II.
 CC Interpro: IPR00559; Hematopo_receptor_L_F2.
 CC Pfam: PFO0041; fn3.3.
 CC SMART: PS01353; HEMATOPO_REC_L_F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
 CC SIGNAL: 1 821 POTENTIAL.
 CC FT SIGNAL 1 821 POTENTIAL.
 CC FT DOMAIN 21 874 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 625 641 POTENTIAL.
 CC FT DOMAIN 642 862 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 224 306 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 421 508 FIBRONECTIN TYPE-III 2.
 CC FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3. (POTENTIAL).
 CC FT CARBOHYD 129 139 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 166 166 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 271 271 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 347 347 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 376 376 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 480 480 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC SEQUENCE 862 AA; 97134 MW; 67C6DD3468BDB8 CRC64;
 CC
 CC Query Match 45.2%; Score 65.5; DB 1; Length 862;
 CC Best Local Similarity 50.0%; Pred. No. 0.03%;
 CC Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
 CC
 CC 1 PEKRNLSITVNECKMGKMGGR 25
 CC
 CC DB 124 PEPPONLSICNGEGVACTMERGR 149
 CC
 CC RESULT 5
 CC IL12B_MOUSE STANDARD: PRT: 874 AA.
 CC AC P93378
 CC DT 20-AUG-2001 (Rel. 40, Created)
 CC DT 20-AUG-2001 (Rel. 40, Last sequence update)
 CC DE 20-AUG-2001 (Rel. 40, Last annotation update)
 CC DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-
 CC 2) (IL-12R-BETA2).
 CC OR IL12RB2.
 CC CC Eukaryotic (Mammal).
 CC CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 CC OX [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=97088510; PubMed=8943050;
 CC PESTREY D.R., Yang H., Minicelli L.J., Chua A.O., Nabavi N., Wu C.-Y.,
 CC Radeley M.R., Gubler U., et al. 1995. The human IL-12 receptor complex is composed of two
 CC beta-type cytokine receptor subunits.*

RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
 CC LOW AFFINITY.
 CC -1- SUPRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC
 CC EMBL: U64199; AA33676.1;
 CC HSP: P40189; IBOU.
 CC Interpro: IPR002966; CIA.
 CC MCD: MCI1270861; IL12rb2.
 CC Interpro: IPR001777; FN.II.
 CC Interpro: IPR00559; Hematopo_receptor_L_F2.
 CC Pfam: PFO0041; fn3.4.
 CC SMART: PS01354; HEMATOPO_REC_L_F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
 CC SIGNAL: 1 20
 CC FT SIGNAL 1 20
 CC FT DOMAIN 21 874 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 657 872 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 657 872 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 137 230 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 240 322 FIBRONECTIN TYPE-III 2.
 CC FT DOMAIN 436 523 FIBRONECTIN TYPE-III 3.
 CC FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.
 CC FT CARBOHYD 48 48 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 101 101 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 116 116 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 142 142 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 151 151 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 169 169 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 179 179 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 224 224 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 232 232 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 267 267 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 287 287 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 323 323 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 391 391 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 495 495 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC SEQUENCE 874 AA; 98196 MW; 5824D21B1F9D67 CRC64;
 CC
 CC Query Match 43.8%; Score 63.5; DB 1; Length 874;
 CC Best Local Similarity 44.4%; Pred. No. 0.07%;
 CC Matches 12; Conservative 6; Mismatches 9; Indels 3; Gaps 2;
 CC
 CC 1 PEKRNLSITVNECKMGK -MGKMGGR 25
 CC
 CC DB 137 PEPPONLSICNGEGVACTMERGR 162
 CC
 CC RESULT 6
 CC IL12F_MOUSE STANDARD: PRT: 1092 AA.
 CC AC P42703;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 15-JUL-1995 (Rel. 36, Last annotation update)
 CC DE IL-12 RECEPTOR BETA-2 CHAIN PRECURSOR (ILF-R) (D-FACTOR/ILF
 CC RECEPTOR).

[illegible][illegible]

[illegible]

Query Match 36.9% Score 53.5 DB 1; Length 837;
 Similarity 33.8%; Predict. No. 11;
 Matches 9; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
 Oy 1 PERKINSCTIVN-EGRKRCMDCG 24
 124 PASPSNLSCTMLHTTNSLYCOWERG 148

RESULT 10

PRLR.COLL: STANDARD: PRT: 830 AA.

AC 090374;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 01-JUN-1994 (Rel. 29, Last annotation update)
 PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Archosaustra; Aves; Neognathae; Columbiformes; Columidae; Columba.
 NCBI_TaxId=9932;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=428567; PubMed=7516866;
 RA Chen X., Horsman N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor".
 RL Endocrinology 135:269-276(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBROBLAST TYPE III-LIKE DOMAINS.

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 CC EMBL: U07694; AAA20646.1;
 CC HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR001573; FN.II.
 DR Pfam: PF00041; fn3.4.
 DR SMART: SM00060; FN3.4.
 DR PROSITE: PS01352; HEMATOPOI_REC_L.F1; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT PROBLEM 24 439
 FT DOMAIN 461 830
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 53 86
 FT CARBOHYD 53 86
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316

FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT PROBLEM 24 439
 FT DOMAIN 461 830
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 53 86
 FT CARBOHYD 53 86
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316

FT CARBOHYD 336 336
 SO SEQUENCE 830 AA; 94507 MW; 38074E830DF695EFF CRC64;
 Query Match 33.8% Score 49; DB 1; Length 830;
 Similarity 39.3%; Predict. No. 11;
 Matches 11; Conservative 2; Mismatches 11; Indels 4; Gaps 1;
 Oy 1 PERKINSCTIVNEGRKRCMDCG 24
 232 PERKINSCTIVNEGRKRCMDCG 259

RESULT 11

PRLR.COLL: STANDARD: PRT: 831 AA.

AC 004594;
 01-JUN-1994 (Rel. 29, Created)
 01-JUN-1994 (Rel. 29, Last sequence update)
 15-JUL-1998 (Rel. 35, Last annotation update)
 PROLACTIN RECEPTOR PRECURSOR (PRL-R) (cPRLP).
 GN
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 NCBI_TaxId=9031;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=WHITE LEGHORN; TISSUE=Kidney;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence".
 RL Biochem Biophys Res Commun 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBROBLAST TYPE III-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and usage by and for commercial purposes is not intended. See <http://www.isb.sdb.ch/announce/> or send an email to license@sdb.sdb.ch.
 CC EMBL: U13154; AAA02439.1;
 CC HSSP: P16475; 1J0655.
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR001777; FN.II.
 DR Pfam: PF00041; fn3.4.
 DR SMART: SM00060; FN3.4.
 DR PROSITE: PS01352; HEMATOPOI_REC_L.F1; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT DOMAIN 439 831
 FT TRANSMEM 460 831
 FT DOMAIN 123 222
 FT DOMAIN 229 325
 FT DOMAIN 326 428
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100

FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT DOMAIN 439 831
 FT TRANSMEM 460 831
 FT DOMAIN 123 222
 FT DOMAIN 229 325
 FT DOMAIN 326 428
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100

[illegible][illegible]

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RESULT 2
ID O9B6G9 PRELIMINARY: PRT: 518 AA.
AC O9B6G9
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GLYCOPROTEIN 130 PRECURSOR.
DS 130
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NC NCBL_TaxID=9031.
RN 1
RS SOURCE FROM N.A.
SC TISSUE=EMBRYOIC; HEART PRIMARY CULTURE (E7, E8);
EX MEDLINE=99026068; PubMed=9906927;
RA Gelsen M., Heller S., Penhale D., Embarger U., Rohrer H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
on gpl30 cytokine receptor signaling."
PM Development 125:4791-4801 (1998).
DE EMBL: AJ016888; C9482084.1; -.
DS 1
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003529; Hematopo_receptor_L.F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L.F2; UNKNOWN.1.
FM SIGNAL.
FT CHAIN.
FT SIGNAL.
SEQUENCE 918 AA: 102495 MW; FE7625F3FE3613ER CRC64;

Query Match 55.9%; Score 81; DB 13; Length 918;
Best Local Similarity 58.6%; Pred. No. 0.00077;
Matches 17; Conservative 1; Mismatches 7; Indels 4; Gaps 1;
OY 1 PERKINSCITYNECK--MRCNDGCR 25
DB 129 PERKINSCITYNECK--MRCNDGCR 157

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Query Match 53.8%; Score 78; DB 13; Length 881;
Best Local Similarity 52.0%; Pred. No. 0.0021;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 1 PERKINSCITYNECK--MRCNDGCR 25
DB 122 PERKINSCITYNECK--MRCNDGCR 146

RESULT 4
ID O9B6G2 PRELIMINARY: PRT: 861 AA.
AC O9B6G2
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE IL-12 RECEPTOR BETA2 PRECURSOR.
GN IL-12R BETA2
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NC NCBL_TaxID=9913.
RN 1
RS SOURCE FROM N.A.
SC TISSUE=LYMPH NODE;
RA Waldvogel A.S., Zakher A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL: AJ308428; CAC28320.1; -.
DS 1
DR Signal: Receptor.
FM SIGNAL.
FT CHAIN.
FT SIGNAL.
SEQUENCE 861 AA: 96208 MW; 4B7B1E501B358E5B CRC64;

Query Match 44.5%; Score 64.5; DB 6; Length 861;
Best Local Similarity 48.1%; Pred. No. 0.22;
Matches 13; Conservative 6; Mismatches 5; Indels 3; Gaps 2;
OY 1 PERKINSCITYNECK--MRCNDGCR 25
DB 124 PERKINSCITYNECK--MRCNDGCR 149

RESULT 5
ID O9B8Z1 PRELIMINARY: PRT: 970 AA.
AC O9B8Z1
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ONCOSTATIN M RECEPTOR BETA.
OS OSMR.
NC NCBL_TaxID=10090.
RN 1
RS SOURCE FROM N.A.
SC TISSUE=LYMPH NODE;
RA Miyajima A.;
RA Tanaka M., Hara T., Copeland N.G., Gilbert D.J., Jenkins N.A.;
RT Structure of the mouse oncostatin M (OSM) receptor: molecular cloning
and functional analysis.
DE EMBL: U00000; C9482084.1; -.
DS 1
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003529; Hematopo_receptor_L.F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 3.

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Search completed: December 19, 2001, 16:25:24
Job time: 549 sec

Thu Dec 20 08:57:59 2001

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:00 ; Search time 78.52 Seconds
(without alignments)
7.165 Million cell updates/sec

Title: US-09-202-104a-7

Perfect score: 145
Sequence: 1 PEKFNLSCTVNGKKKRCMGGR 25

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212352 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212352

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, MA: *
1: /cgn2.6/pdata/2/1aa/5A.COMB.pep: *
2: /cgn2.6/pdata/2/1aa/5B.COMB.pep: *
3: /cgn2.6/pdata/2/1aa/6A.COMB.pep: *
4: /cgn2.6/pdata/2/1aa/6B.COMB.pep: *
5: /cgn2.6/pdata/2/1aa/PCFUS.COMB.pep: *
6: /cgn2.6/pdata/2/1aa/BACKLIST1.pep: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	488	2	US-08-599-455B-5
2	145	100.0	488	2	US-08-599-455B-5
3	145	100.0	572	2	US-08-419-652-5
4	145	100.0	658	2	US-08-825-558-4
5	145	100.0	708	1	US-07-787-586-2
6	145	100.0	708	1	US-08-058-264-2
7	145	100.0	708	2	US-09-059-099-2
8	145	100.0	708	3	US-09-058-264-2
9	145	100.0	708	5	PCF-US99-06530-2
10	145	100.0	918	2	US-08-825-558-6
11	145	100.0	918	2	US-08-825-558-6
12	145	100.0	918	2	US-08-825-558-6
13	145	100.0	918	2	US-08-825-558-6
14	145	100.0	918	2	US-08-825-558-6
15	145	100.0	918	2	US-08-825-558-6
16	145	100.0	918	2	US-08-825-558-6
17	145	100.0	918	2	US-08-825-558-6
18	145	100.0	918	2	US-08-825-558-6
19	145	100.0	918	2	US-08-825-558-6
20	145	100.0	918	2	US-08-825-558-6
21	145	100.0	918	2	US-08-825-558-6
22	145	100.0	918	2	US-08-825-558-6
23	145	100.0	918	2	US-08-825-558-6
24	145	100.0	918	2	US-08-825-558-6
25	145	100.0	918	2	US-08-825-558-6
26	145	100.0	918	2	US-08-825-558-6
27	145	100.0	918	2	US-08-825-558-6

28	63	43.4	392	4	US-09-071-224-18	Sequence 18, App1
29	63	43.4	422	4	US-09-071-224-2	Sequence 2, App1
30	63	43.4	425	4	US-09-071-224-4	Sequence 4, App1
31	63	43.4	434	3	US-09-072-024-4	Sequence 4, App1
32	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
33	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
34	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
35	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
36	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
37	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
38	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
39	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
40	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
41	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
42	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
43	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
44	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1
45	63	43.4	434	4	US-09-120-601-6	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; PRIORITY: 08/599,455
; GENERAL INFORMATION:
; INVENTOR: Thompson, Robert I. A.
; APPLICANT: Clapper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSD for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/569,145
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/566,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/562,663
; ATTORNEY/AGENT INFORMATION:
; NAME: Melillo, Ph.D., Anita L.
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-5070
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455a-5

Query Match 100.0%; Score 145; DB 2; Length 488;

Best Local Similarity 100.0%; Pred.No.1.5e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-069-761B-5

Sequence 5, Application US/09069761B

Patent No. 628/782

GENERAL INFORMATION:

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

MOLECULE TYPE: protein
US-09-069-761B-5

Query Match 100.0%; Score 145; DB 4; Length 488;

Best Local Similarity 100.0%; Pred.No.1.5e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-419-652-5

Sequence 5, Application US/08419652

Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

MOLECULE TYPE: protein
US-09-069-761B-5

Query Match 100.0%; Score 145; DB 2; Length 488;

Best Local Similarity 100.0%; Pred.No.1.5e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-419-652-5

Sequence 5, Application US/08419652

Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

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APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

APPLICANT: GIBBIER, ULLICH A.

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RESULT 4
US-08-825-558-4
Sequence 4, Application US/08825558
Patent No. 5565724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 4
INVENTOR: SHARKEY, ANDREW
ADDRESS: STEPHEN KESSLER, GOLDSTEIN & FOX
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
FILING DATE: 19-MAR-1997
CLASSIFICATION: 356
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,893
NAME: ESMOND, ROBERT W.
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-4

Query Match
Best Local Similarity 100.0%
Seq No. 2a-13: 0
Matches 25: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PERKINSCITVNBCKKMKCMDCGR 25
|||||
Db 126 PERKINSCITVNBCKKMKCMDCGR 150

RESULT 5
US-07-797-556-2
Sequence 2, Application US/0797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OR INVENTION: Receptor for Oncostatin M and Leukemia
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match
Best Local Similarity 100.0%
Seq No. 2a-13: 0
Matches 25: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PERKINSCITVNBCKKMKCMDCGR 25
|||||
Db 126 PERKINSCITVNBCKKMKCMDCGR 150

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 356
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match
Best Local Similarity 100.0%
Seq No. 2a-13: 0
Matches 25: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PERKINSCITVNBCKKMKCMDCGR 25
|||||
Db 126 PERKINSCITVNBCKKMKCMDCGR 150

RESULT 6
US-08-308-881-2
Sequence 2, Application US/0830881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Mosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

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Query Match 100.0%: Score 145; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PEPKRNLSCTVINEGKKRKCNDGGR 25
DB 126 PEPKRNLSCTVINEGKKRKCNDGGR 150

RESULT 7
US-09-058-263-2
Sequence 2, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF INVENTORS: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058.263
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308.881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249.553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REFERENCE/DOCKET NUMBER: 2614-A
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-263-2

RESULT 8
US-09-059-099-2
Sequence 2, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF INVENTORS: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059.264
FILING DATE:

TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059.099
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308.881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249.553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REFERENCE/DOCKET NUMBER: 2614-A
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%: Score 145; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PEPKRNLSCTVINEGKKRKCNDGGR 25
DB 126 PEPKRNLSCTVINEGKKRKCNDGGR 150

RESULT 9
US-09-058-264-2
Sequence 2, Application US/09058264
Patent No. 6010886
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF INVENTORS: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058.264
FILING DATE:

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? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/308,881
? FILING DATE: 26-MAY-1994
? APPLICATION NUMBER: US/08/249,553
? ATTORNEY/AGENT INFORMATION:
? NAME: Seese, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELETYPE: 756822
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 708 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? NO. OF CD: 1
? US-09-055-264-2

Query Match          100.0%; Score 145; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PERKINSCTIVNECKMKRCMDGGR 25
DB 126 PERKINSCTIVNECKMKRCMDGGR 150

RESULT 10
PCT-US95-06530-2
? Sequence 2, Application PC/7059506530
? GENERAL INFORMATION:
? APPLICANT: Cosman, David J.
? TITLE OF INVENTION: Receptor for Oncostatin M
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1, Version #1.30
? APPLICATION NUMBER: US/95/06530
? CURRENT APPLICATION DATA:
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/308,881
? FILING DATE: 26-MAY-1994
? APPLICATION NUMBER: US/08/249,553
? ATTORNEY/AGENT INFORMATION:
? NAME: Anderson, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-MO
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELETYPE: 756822
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 708 amino acids
? TYPE: amino acid

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? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PCT-US95-06530-2

Query Match          100.0%; Score 145; DB 5; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PERKINSCTIVNECKMKRCMDGGR 25
DB 126 PERKINSCTIVNECKMKRCMDGGR 150

RESULT 11
US-08-825-558-6
? Sequence 6, Application US/0825558
? Patent No. 5965724
? GENERAL INFORMATION:
? APPLICANT: SHARKEY, ANDREW
? ATTORNEY/AGENT INFORMATION:
? NAME: SHARKEY, ANDREW K.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 0623.0530001
? TELEPHONE: (202)371-2600
? TELEFAX: (202)371-2640
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 918 amino acids
? TYPE: amino acid
? MOLECULE TYPE: protein
? US-08-825-558-6

Query Match          100.0%; Score 145; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 2,9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PERKINSCTIVNECKMKRCMDGGR 25
DB 126 PERKINSCTIVNECKMKRCMDGGR 150

RESULT 12
US-08-684118-2
? Sequence 2, Application US/08685118
? Patent No. 5840510
? GENERAL INFORMATION:
? APPLICANT: Gubler, Ulrich A.
? ATTORNEY/AGENT INFORMATION:
? NAME: Gubler, David H.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 0623.0530001
? TELEPHONE: (202)371-2600
? TELEFAX: (202)371-2640
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 918 amino acids
? TYPE: amino acid

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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: La Roche Inc.
ADDRESS: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2863
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13; 8; Indels 1; Gaps 1;
Matches 13; Conservative

QY 1 PERKINSCT-VNEGKMKRCMDGCR 25
DB 124 PRQPNLSCTGKGGVACTWCKR 149

RESULT 13
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9132
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682

REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2863
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13; 8; Indels 1; Gaps 1;
Matches 13; Conservative

QY 1 PERKINSCT-VNEGKMKRCMDGCR 25
DB 124 PRQPNLSCTGKGGVACTWCKR 149

RESULT 14
US-08-914-520-2
Sequence 2, Application US/0891520
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9135
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2863
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-914-520-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13; 8; Indels 1; Gaps 1;
Matches 13; Conservative

QY 1 PERKINSCT-VNEGKMKRCMDGCR 25
DB 124 PRQPNLSCTGKGGVACTWCKR 149

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RESULT 15
US-09-071-224-21
US-09-071-224-21 Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: LOK, SI
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Jansen, Robert
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS Windows Version 2.0
SEQUENCE FRAMES FOR Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/071,224
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
INFORMATION FOR SEQ. ID NO. 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE type: Protein
US-09-071-224-21

Query Match 43.4%; Score 63; DB 4; Length 303;
Best Local Similarity 45.8%; Pred. No. 0.094;
Matches 11; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
QY 1 PERKINSCTVNEGKMKRCMDGQ 24
Db 98 PERPVNISCNKNKNDICMKTPG 121

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Job time: 406 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:35 ; Search time 170.68 Seconds
(without alignments)
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Title: us-09-202-104a-8

Sequence: 1 NFIILKSNMATHKFAICKAKRPPYS 25

Scoring table:

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Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 08
Maximum Match 1008
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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2	139	100.0	180	17 AAM00404	Interleukin-6 anta
3	139	100.0	329	18 AAM17859	Rheumatoid arthrit
4	139	100.0	332	20 AAM70799	Human gp130-beta
5	139	100.0	332	21 AAY92188	Human gp130-beta
6	139	100.0	332	21 AAY92187	Human gp130-beta
7	139	100.0	708	14 AAY37860	Human gp130 N-term
8	139	100.0	708	17 AAB59184	Human gp130 N-term
9	139	100.0	727	21 AAY92182	Human gp130-Kappa
10	139	100.0	738	21 AAY92182	Human gp130-Kappa
11	139	100.0	859	20 AAM70796	Human gp130-PC-His

12	139	100.0	859	21 AAY92184	Human gp130-PC-His
13	139	100.0	918	12 AAR10545	Recombinant human
14	139	100.0	918	15 AAR46233	Human soluble glyco
15	139	100.0	918	17 AAR46238	Human gp130 protei
16	139	100.0	951	21 AAM70798	Human gp130-C-gam
17	139	100.0	951	21 AAM70798	Human gp130-C-gam
18	139	100.0	951	21 AAY92186	Human gp130-C-gam
19	139	100.0	951	21 AAY92187	Human gp130-C-gam
20	139	100.0	1158	21 AAY92205	Fusion polypeptide
21	139	100.0	1158	21 AAY92205	Fusion polypeptide
22	118	84.9	24	22 AAB88833	Human Interleukin-
23	102	73.4	24	22 AAB88832	Human Interleukin-
24	88	63.3	917	21 AAY50723	Human gp130 muscu
25	88	63.3	917	21 AAY50723	Human gp130 muscu
26	61	43.9	24	22 AAB88834	Human Interleukin-
27	50	36.0	27	27 AAM81867	Human tumour supp
28	46	33.1	24	22 AAB88831	Human Interleukin-
29	46	33.1	592	17 AAR86914	xylinase XYNB. No
30	45.5	32.7	436	20 AAR37223	Protein involved i
31	45.5	32.7	563	21 AAG47223	Arabiopsis thalia
32	45.5	32.7	563	21 AAG47223	Arabiopsis thalia
33	45.5	32.7	585	21 AAG45221	Arabiopsis thalia
34	45	32.4	286	21 AAG39454	Arabiopsis thalia
35	45	32.4	292	21 AAG39454	Arabiopsis thalia
36	45	32.4	369	22 AAG39454	C glutamic prote
37	44	31.7	2410	18 AAM19723	Cell cycle checkpo
38	44	31.7	2480	18 AAM19723	Cell cycle checkpo
39	44	31.7	2544	26 AAM19724	Human alpha and r
40	44	31.7	2544	26 AAM19724	Human alpha and r
41	43	30.9	10	22 AAB49032	gp130-derived back
42	43	30.9	328	21 AAB18899	A maize chitinase
43	43	30.9	339	21 AAB19406	Human polypeptide
44	43	30.9	341	22 AAM40059	Human polypeptide
45	43	30.9	369	22 AAM41845	Human polypeptide

ALIGNMENTS

RESULT 1
AAM52208 standard; peptide; 25 AA.
ID AAM52208
AC AAM52208
XX 09-JUN-1996 (first entry)
DE Interleukin-6 antagonist peptide.
KW Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW acquired immune deficiency syndrome-related lymphoma; immune response;
KW rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW Alzheimer's disease.
XX Synthetic.
OS Home sapiens.
XX MO9748728-A1.
XX 24-DEC-1997.
XX 19-JUN-1997; 97NO-WL00345.
XX 20-JUN-1996; 96EP-0201720.
XX (KOSTV) KOSTER H W.
XX Hoebe KRN, Van Leengoed LAMG;
XX WPI. 1996-063080/06.
XX New peptide(s) with interleukin-6 agonist or antagonist activity -
XX useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 XX
 PS
 CC Claim 6; Page 17; 28pp; English.
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6-related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome, osteoporosis, Alzheimer's disease etc.) also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC cytotoxic, do not suppress the immune system, do not cause hepatitis, or
 CC hepatocytosis) contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 XX Sequence 25 AA:
 SO
 Query Match 100.0%; Score 139; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NFKLSEMTKTRFACKAKRDTPTS 25
 Db 1 nfksewathkackardtpts 25
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 AA0004
 ID AA000404 standard; peptide; 180 AA.
 XX AA000404;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DB Interleukin-6 antagonist peptide.
 XX
 XX IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PM JP07324097-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 30-MAY-1994; 94AP-0111259.
 XX
 PP 30-MAY-1994; 94JP-0111259.
 XX
 PR (DAIIC) DAICEL CHEM IND LTD.
 XX
 PA (FUJII) FUJISAWA PHARM CO LTD.
 XX
 DR WPI: 1996-065476/07.
 XX
 XX Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 PS Claim 1; Page 2; 19pp; Japanese.
 XX
 XX New IL-6 antagonists are provided which are of formula x-w-y, in
 CC which x is H or an amino-protecting group, y is OH or a carboxy-
 CC protecting group, and w is a peptide containing all or part of the
 CC sequence as given in AA000402, AA000403 or AA000404 (the
 CC present sequences), where any free metcipo groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from
 CC the present sequence (AA000436 - AA000442) are claimed as special
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 CC
 XX Sequence 180 AA:
 SO
 Query Match 100.0%; Score 139; DB 17; Length 180;
 Best Local Similarity 100.0%; Pred. No. 9.2e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NFKLSEMTKTRFACKAKRDTPTS 25
 Db 35 nfksewathkackardtpts 59
 RESULT 3
 AA017859
 ID AA017859 standard; Protein; 329 AA.
 XX AA017859;
 XX
 DT 04-FEB-1998 (first entry)
 XX
 DB Rheumatoid arthritis auto-antigen clone A.
 XX
 XX Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
 KW prediction; synovial cell.
 XX
 OS Homo sapiens.
 XX
 PM W09717441-A1.
 XX
 PD 15-MAY-1997.
 XX
 PF 06-NOV-1996; 96WO-JP03250.
 XX
 PP 07-NOV-1995; 95JP-0286957.
 XX
 PR (KANF) KANEXA CORP.
 XX
 PA Kishimura M, Nakao K, Osaka F, Osaki S, Tanaka M;
 PI WPI: 1997-281030/25.
 XX
 DR N-PSDB; AAT88830.
 XX
 XX Auto-antigen from synovial cells of rheumatoid arthritis patients -
 PT binds to antibodies present in these patients, for diagnosis and
 PT prediction of the disease
 XX
 PS Claim 3; Pages 36-37; 61pp; Japanese.
 XX
 XX The present sequence is the rheumatoid arthritis (RA) auto-antigen
 CC clone A, which can be used to diagnose and predict the development
 CC of RA. The clone A is a polypeptide chain of 180 amino acids. The
 CC sera from patients with RA contain antibodies in biological specimens, e.g.,
 CC RNA was isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using 195 separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression on
 CC vector for the transformation of E. coli M522. Transforms on
 CC culture express clone A peptide and folistatin related protein
 CC into the culture medium.
 XX
 XX
 SO Sequence 329 AA:
 Query Match 100.0%; Score 139; DB 18; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.0e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NFKLSEMTKTRFACKAKRDTPTS 25

DB 157 nfkiksewacknfadckakrdcpis 181

RESULT 4

AAW70799 standard; protein; 332 AA.

AAW70799;

03-FEB-1999 (first entry)

Human gp130-delta-3fibro amino acid sequence.

gp130: cytokine antagonist; interleukin; gamma-interferon; granulocyte macrophage colony-stimulating factor; J peptide; transforming growth factor-beta.

Synthetic.
Homo sapiens.

Key Location/Qualifiers
Protein 1..330
/note="human gp130"

US5844099-A.

01-DEC-1998.

27-NOV-1995: 9505-0563105.

27-NOV-1995: 9505-0563105.

20-OCT-1993: 9305-0140222.

(REG-) REGENERON PHARM INC.

Economides A, Stahl N, Yancopoulos GD;

WPI: 1999-044669/04.

Cytokine antagonists - comprising extracellular domains of specifically-determining and signal-transducing components of cytokine receptor

Example 4; Fig 10; 46pp; English.

The present sequence represents the amino acid sequence of human gp130-delta-3fibro. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specifically-determining component of the cytokine receptor and the extracellular domain of the cytokine receptor. The invention also provides a fusion polypeptide which is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines.

Sequence 332 AA;

Query Match 100.0%; Score 139; DB 20; Length 332;

Best Local Similarity 100.0%; Pred. No. 1,8e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

AAV92188 standard; protein; 332 AA.

AAV92188;

01-AUG-2000 (first entry)

Human gp130-delta-3fibro.

gp130-delta-3fibro: cytokine; antagonist; CNTF; receptor; fusion protein; cytoskeletal; immunomodulator; osteopathic.

Synthetic.
Homo sapiens.

Key Location/Qualifiers
Protein 1..330
/label="gp130"
Peptide 331..332
/note="Ser-Gly bridge"

W0200018932-A2.

06-APR-2000.

22-SEP-1999: 99NO-US22045.

25-SEP-1998: 98US-0101858.

15-MAY-1999: 99US-0313942.

(REG-) REGENERON PHARM INC.

Stahl N, Yancopoulos GD;

WPI: 2000-293165/25.

Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex

Example 4; Fig 10; 152pp; English.

The invention concerns production of antagonists to any cytokine that binds to a specific receptor. The invention provides a fusion polypeptide with the extracellular domain of the cytokine receptor and the extracellular domain of a non-functional intermediate which binds to a second beta signal transducing component causing beta-receptor dimerization. The soluble alpha specifically determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (SR-alpha-beta-1) that act as antagonist to the cytokine receptor. The invention also provides a fusion polypeptide which is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines.

Sequence 332 AA;

Query Match

Best Local Similarity 100.0%; Score 139; DB 21; Length 332;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NPTLKSEVATHRFADCAKAROTPTS 25
 DB 157 nftlksevathtkacacaktidpts 181

RESULT 6
 AAR94576
 ID AAR94576 standard: Protein: 658 AA.
 XX AAR94576:
 DT 20-JUN-1996 (first entry)
 DE Human gp130 splice variant.
 XX Gp130; transmembrane domain; growth factor antagonist;
 XX embryo preimplantation; in vitro fertilisation.
 XX Homo sapiens.
 XX MO9609382-AL.
 XX 28-MAR-1996.
 XX 21-SEP-1995: 95MO-G802243.
 XX 21-SEP-1994: 94GB-0019021.
 XX (ISTE) ARS APPLIED RES SYST HOLDING NV.
 XX Dellow KA, Sharkey A, Smith SK:
 DR WPI: 1996-188444/19.
 DR N-PSDB: AAT14602.
 XX
 XX New splice variant of gp130 lacking the trans-membrane domain
 PF useful as an antagonist for growth factors esp. for ensuring correct
 PF development of pre-implantation embryos
 PP
 PP Example 2: Fig 1: 33pp: English.
 CC A novel, soluble splice variant (AAR94576) of human gp130 corresponds
 CC to amino acids 1-613 of native gp130 (AAR5368) but has a novel
 CC C-terminal sequence (AAR94575) from amino acid 614 onwards.
 CC The splice variant lacks a transmembrane region. It was initially
 CC detected during the morula to blastocyst transition of human
 CC embryos. The splice variant antagonises the action of growth
 CC factors such as transforming growth factor- β and oncofetal protein.
 CC oncofetal M and interleukin-11 and can be used to generate correct
 CC development of preimplantation embryos" partic. for in vitro
 CC fertilisation.
 CC
 SO Sequence 658 AA:

Query Match 100.0%; Score 139; DB 17; Length 658;
 Best Local Similarity 100.0%; Pred. No. 3 76-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NPTLKSEVATHRFADCAKAROTPTS 25
 DB 157 nftlksevathtkacacaktidpts 181

RESULT 7
 AAR37804
 ID AAR37804 standard: Protein: 708 AA.
 XX AAR37804:
 AC
 XX
 XX .01-OCT-1993 (first entry)

XX Human gp130 N-terminal fragment.
 DE
 XX Oncofetalin M; leukaemia inhibitory factor; receptor; PCR; fusion;
 XX LIF-R; gp130; linker.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 1..22 /label= s1g-peptide
 FH Peptide 23-708
 FH Protein /label= mat_protein
 FH Domain 23..619
 FH /label= extracell_jlar_domain
 FH Region 620
 FH /label= transmembrane_region
 FH /note= "beginning with amino acid 620"
 FH Domain 620-708
 FH /label= cytoplasmic_domain
 FH /note= "partial cytoplasmic domain"
 FH Misc-difference 8 /note= "differs from the equiv. portion of the Hbl1
 FH et al. Cell 63:1149 (1990) protein in that
 FH the eighth amino acid of the signal sequence
 FH is leu rather than val"
 XX
 XX MO9310151-A.
 XX 27-MAY-1993.
 XX 20-NOV-1992: 92MO-US10272.
 XX 22-NOV-1991: 91US-0797556.
 XX (IMWV) IMMUNEX CORP.
 XX
 XX Gearing DP;
 XX WPI: 1993-182493/22.
 XX N-PSDB: AAO42586.
 XX
 XX Receptor protein comprising gp130 covalently linked to LIF
 PF receptor - binds to oncofetalin M and LIF useful for treating
 PF Kaposi's sarcoma, atherosclerosis, obesity etc.
 PP
 PP Disclosure: Page 48-53: 79pp: English.
 CC A new receptor (R), able to bind oncofetalin M and leukaemia
 CC inhibitory factor (LIF) gp130 polypeptide (AAO42586)
 CC covalently coupled to LIF-receptor (LIF-R) (AAO42590); for example
 CC suitable gp130 polypeptides comprise amino acids 22-528, 22-320,
 CC 120-320 etc., or lack all or part of the transmembrane region
 CC and/or cytoplasmic domain.
 CC Pref. both components of (R) are soluble proteins and are connected
 CC by a polypeptide linker of 20-100 amino acids consisting of Gly, Asn,
 CC Ser, Thr or Ala.
 CC
 SO Sequence 708 AA:

Query Match 100.0%; Score 139; DB 14; Length 708;
 Best Local Similarity 100.0%; Pred. No. de-13; 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NPTLKSEVATHRFADCAKAROTPTS 25
 DB 157 nftlksevathtkacacaktidpts 181

RESULT 8
 AAR85911

[illegible]

	CX	polypeptides, where an antibody Fc region is joined to the C-terminus of each of the soluble proteins.
	CC	In this case, the two fusion polypeptides are joined by disulfide bonds between the two antibody Fc regions.
	CC	The heterodimeric receptors can be used to inhibit biological activities mediated by oncocalcin M.
	CC	The advantage with using the heterodimeric receptor construct is that they bind to oncocalcin M at greater levels than gp130 does alone.
SQ	Sequence	708 AA:
DY	Query Match	100.0%; Score 139; DB 17;
DE	Best Local Similarity	100.0%; Pred. No. 4e+13;
KW	Matches 23;	Conservative 0; Mismatches 0; Gaps 0
OY	1 NPTLKSEMAHREPKDKANKRPPTS 25 Db 157 nftlksewathkadeokdrtpcs 181	
XX	RESULT_9	
XN	AAY92192	
XC	AAY92192 standard; protein; 727 AA.	
AC	AAY92192;	
XX	01-AUG-2000 (first entry)	
DT	human gp130-kappa domain fusion protein.	
DE	gp130-kappa domain; cytokine; antagonist; CNTR; receptor; fusion protein; cytosolic; immunomodulator; osteopontin;c. Synthetic.	
OS	Homo sapiens.	
XX	Key Location/Qualifiers	
FH	Protein 1..620	
FT	/label= "gp130"	
FT	Peptide 620..621	
FT	/note= "Ser-gly bridge"	
FT	Protein 622..727	
FT	/label= "IgG_kappa_domain"	
NX	MO2000I0893Z_A2.	
PD	06-APR-2000.	
PP	22-SEP-1999; 99NO-US22045.	
PR	25-SEP-1998; 98US-O101B58.	
PR	19-MAY-1999; 98US-OJ31942.	
RK	(REFE-) REGENERON PHARM INC.	
PI	Stahl N., Yancopoulos GD;	
DR	WPI: 2000-293165/25.	
XX	Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex	
PS	Example 4; Page - : 15ppr; English.	
CC	The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then undergoes a section beta cleavage event resulting in a functional cytokine receptor dimer. The said alpha specificity determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to	

CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine receptor component. The heterodimer is a non-functional complex.
 CC Receptor component are shared by cytokines such as the CNTF (cellular
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the alpha receptor and the beta-1 receptor.
 CC Components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides such as osteoporosis and primary and secondary effects of
 CC cancer, including multiple myeloma or cachexia.
 CC Sequences are constructed from the gp130 and kappa domain
 CC sequences given in figures 9 and 11 of the specification.

Sequence 727 AA:

Query Match 100.0%: Score 139; DB 21; Length 727;
 Best Local Similarity 100.0%: Pred. No. 4,1e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NPTLKSBNATKRFACCKAKRDTPTS 25
 Db 157 nftlksewathktdckakrtdpts 181

RESULT 10

AAV92194 standard; protein: 738 AA.

AAV92194:

01-AUG-2000 (first entry)

Human gp130-J-kappa fusion protein.

gp130-J-kappa: cytokine; antagonist; CNTF; receptor; fusion protein;
 cytosolic; immunomodulator; osteopathic.

Synthetic.

Homo sapiens.

Key

Protein

Peptide

Peptide

Domain

WO200018332-A2.

06-APR-2000.

22-SEP-1999. 59M0-0522045.

25-SEP-1998. 98M0-0101858.

19-MAY-1999. 99M0-0313942.

(REG-) REGENERON PHARM INC.

Stahl M, Yancopoulos GD.

WPI: 2000-253165/75.

FF Isolated nucleic acid molecule for treating cytokine-related diseases
 FF or disorders involving a fusion polypeptide capable of binding a cytokine
 FF to form a nonfunctional complex.
 XX
 PS Example 4; Page 7; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional complex.
 CC signal transducing component causing beta-receptor dimerization the
 CC soluble alpha specificity determining component of the receptor.
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC heterodimer components are shared by cytokines such as the CNTF (cellular
 CC neurotrophic factor) family of cytokines.
 CC The invention provides the basis for the development of IL-6 antagonists as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha and the beta-1 receptor.
 CC Components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

Sequence 738 AA:

Query Match 100.0%: Score 139; DB 21; Length 738;
 Best Local Similarity 100.0%: Pred. No. 4,2e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NPTLKSBNATKRFACCKAKRDTPTS 25
 Db 157 nftlksewathktdckakrtdpts 181

RESULT 11

AAV0796 standard; protein: 859 AA.

AAV0796:

03-FEB-1999 (first entry)

Human gp130-Fc-His6 amino acid sequence.

gp130: cytokine antagonist; interleukin; gamma-interferon;
 granulocyte macrophage colony-stimulating factor; J peptide;
 transforming growth factor-beta.

Synthetic.

Homo sapiens.

Key

Protein

Peptide

Peptide

Domain

WO200018332-A2.

06-APR-2000.

22-SEP-1999. 59M0-0522045.

25-SEP-1998. 98M0-0101858.

19-MAY-1999. 99M0-0313942.

(REG-) REGENERON PHARM INC.

Stahl M, Yancopoulos GD.

WPI: 2000-253165/75.

FT		/note= "from the Fc domain of human IgG1"
FT	Disulfide-bond	632..635
FT	Peptide	854..859
FT		/note= "hexahistidine tag"
XX		
XX	US5644039-A.	
XX		
XX	01-DEC-1998.	
PD		
PF	27-MOV-1995;	9505-0563105.
XX		
PR	27-NOV-1995;	9505-0563105.
XX	20-OCT-1993;	9305-0104222.
XX	(REG-) REGENERON PHARM INC.	
PI	Economides A, Stahl N, Vancopoulos GD;	
DR	WPI; 1999-044669/04.	
XX		
XX	Cytokine antagonists - comprising extracellular domains of	
PT	specifically identifying and signal-transducing components of	
PT	cytokine receptor	
XX		
PS	Example 3; Fig 4; 46pp; English.	
XX		
CC	The present sequence represents the amino acid sequence of human	
CC	gp130-Fc-His6. The protein is used in the course of the invention. The	
CC	extracellular domain of the cytokine receptors comprising only the	
CC	signal-transducing domain of the cytokine receptor is also dependent of	
CC	the cytokine receptor and the extracellular domain of a	
CC	signal-transducing component of the cytokine receptor. The cytokine	
CC	is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),	
CC	granulocyte macrophage colony-stimulating factor (GM-CSF),	
CC	gamma-interferon or transforming growth factor-beta (TGF-beta). The	
CC	antagonist is capable of blocking the cytokine to form a nonfunctional	
CC	complex with the cytokine receptor. The complex is stable in solution	
CC	and can also be used in assays for identifying novel agonists and	
CC	antagonists of cytokines.	
XX		
SQ	Sequence 859 AA:	
	Query Match	100.0%; Score 139; DB 20;
	BlastClust Similarity	100.0%; P < 4e-20;
	Matches 25; Conservative 0; Mismatches 0;	Indels 0; Gaps 0
OY	1 NPFIKSEVNRHFPADCKAKSDTPTS 25	
DB	157 nftkswethkfadckakrdrps 181	
RESULT 12		
AA92184		
AA92184 standard; protein: 859 AA.		
XX	AA92184;	
AC		
DY	01-AUG-2000 (first entry)	
XX		
DD	human gp130-Fc-His6.	
XX		
KM	gp130-Fc-His6; cytokine: antagonist; CMT; receptor; fusion protein;	
XX	cystostatic; immunomodulator; osteopathic.	
OS	Synthetic.	
XX	Romo sapiens.	
FA	Key	Location/Qualifiers
FT	Protein	1 619
FT		/label= gp130
FT	Peptide	1..22
FT		/label= signal-peptide

[illegible]

```

AAR10545
XX AAR10545 standard; Protein: 918 AA.
XX
XX AAR10545:
XX
XX 12-APR-1991 (first entry)
XX
DE Recombinant human gp130 protein.
XX
XX Recombinant human gp130; Interleukin-6; Interleukin-6 receptor;
XX Immunity; Hematopoiesis; Inflammation; Therapy.
XX
XX Homo sapiens.
XX
XX EP11946-A.
XX 06-FEB-1991.
XX
XX 02-AUG-1990: 90BP-0308530.
XX
XX 31-MAY-1990: 90BP-0140069.
XX 03-AUG-1989: 89BP-0200230.
XX
XX (KISHU/) KISHIMOTO T.
XX
XX Kishimoto T.
XX
XX WPI: 1991-038820/06.
XX N-PSDB: AAO10402.
XX
XX Recombinant human gp130 protein - acts in the transmission of
XX Interleukin-6 signal for defence mechanisms
XX
XX Disclosure: fig 7; 32pp: English.
XX
XX This gp130 protein is produced using standard recombinant DNA
XX methods (see AAO10402), free from any other human protein. It
XX participates in the transmission of the Interleukin (IL)-6 sig-
XX nal, and therefore the proliferation and differentiation of an
XX organism. It is important in an animals defence mechanisms, e.g.
XX immunity, hematopoiesis and inflammation.
XX
XX Sequence 918 AA:
XX
Query Match 100.0%; Score 139; DB 12; Length 918;
Best Local Similarity 100.0%; Pred. No. 5,3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NEFTKSNMATHKFKACCKARROTPTS 25
DB 157 nftkswethktdckakrtdpts 181

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XX 02-AUG-1991: 91JP-0217924.
XX
XX 02-AUG-1991: 91JP-0217924.
XX
XX (KISHU/) KISHIMOTO C.
XX (TOYO) TOSOH CORP.
XX
XX WPI: 1994-071006/09.
XX N-PSDB: AAO56931.
XX
XX Preparation of recombinant soluble human gp 130 deriv - for use
XX in the production of anti gp 130 antibody for immunochemical
XX assay
XX
XX Claim 1: Figure 7; 13pp: Japanese.
XX
XX The soluble glycoprotein (gp) 130 can be used as an immunogen for
XX the preparation of anti-gp130 antibody. Soluble gp130 cDNA was prepared
XX by inserting a termination codon prior to the extracellular domain
XX or transmembrane domain of the gp130 coding sequence or simply by
XX eliminating the transmembrane domain.
XX
XX Sequence 918 AA:
XX
Query Match 100.0%; Score 139; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 5,3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NEFTKSNMATHKFKACCKARROTPTS 25
DB 157 nftkswethktdckakrtdpts 181

```

```

RESULT 15
AAR75368
XX AAR75368 standard; Protein: 918 AA.
XX
XX AAR75368:
XX
XX 20-JUN-1996 (first entry)
XX
DE Human gp130 protein.
XX
XX Gp130; transmembrane domain; growth factor antagonist;
XX embryo pre-implantation; in vitro fertilisation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 620..641
XX /label= transmembrane_region
XX
XX M09609382-A1.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995: 95WO-GB02243.
XX 21-SEP-1994: 94GB-0019021.
XX
XX (ISTP) ARS APPLIED RES SYST HOLDING NV.
XX
XX DeJong KA, Sharkey A, Smith SK.
XX WPI: 1996-188444/19.
XX N-PSDB: AAR14603.
XX
XX New splice variant of gp130 lacking the trans-membrane domain
XX useful as an antagonist for growth factors esp. for ensuring correct
XX development of pre-implantation embryos
XX

```


PS Disclosure; Fig 2; 33pp; English.
XX
CC A DNA sequence (AAT14603) codes for native human gp130 (AAR75368).
CC A novel splice variant (see AAT14602) that lacks the transmembrane
CC region was identified in the morula to blastocyst transition stage
CC of human embryos. This variant may antagonizes the action
CC of certain growth factors and can be used to ensure correct
CC development of preimplantation embryos.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 139; DB 17; Length 918;
Identical Similarity 100.0%; Freq. No. 5; Se 13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NPTIKSENAFTKRFADCKAKRDPTPS 25
|||||
Db 157 nftlksewathkfadckakrdptps 181

Search completed: December 19, 2001, 16:19:36
Job time: 361 sec

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GenScore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:39 ; Search time 88.82 seconds

(without alignments)

21.441 million cell updates/sec

Title: US-09-202-104a-8

Perfect score: 139

Sequence: 1 NEFLKSEMAHFKADCKAKRDPIS 25

Scoring table:

BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

pred. No. is the number of results predicted by chance to have a
pred. greater than the observed number of hits being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	918	2	membrane glycoprotein 130
2	88	63.3	917	2	interleukin-6 sign
3	58	63.3	918	2	Ly9c - mouse
4	50	36.0	266	2	hypersplastic discs
5	49	35.3	2895	2	hypothetical protein
6	46.5	33.5	717	2	hypothetical protein
7	46.5	33.5	717	2	hypothetical protein
8	46.5	33.5	717	2	hypothetical protein
9	46.5	33.5	717	2	hypothetical protein
10	46.5	33.5	717	2	hypothetical protein
11	46.5	33.5	717	2	hypothetical protein
12	46.5	33.5	717	2	hypothetical protein
13	46.5	33.5	717	2	hypothetical protein
14	46.5	33.5	717	2	hypothetical protein
15	46.5	33.5	717	2	hypothetical protein
16	46.5	33.5	717	2	hypothetical protein
17	46.5	33.5	717	2	hypothetical protein
18	46.5	33.5	717	2	hypothetical protein
19	46.5	33.5	717	2	hypothetical protein
20	46.5	33.5	717	2	hypothetical protein
21	46.5	33.5	717	2	hypothetical protein
22	46.5	33.5	717	2	hypothetical protein
23	46.5	33.5	717	2	hypothetical protein
24	46.5	33.5	717	2	hypothetical protein
25	46.5	33.5	717	2	hypothetical protein
26	46.5	33.5	717	2	hypothetical protein
27	46.5	33.5	717	2	hypothetical protein
28	46.5	33.5	717	2	hypothetical protein
29	46.5	33.5	717	2	hypothetical protein

30	43	30.9	2303	2	genome polyprotein
31	42.5	30.6	488	2	probable (pel12)
32	42.5	30.6	569	2	thiamin pyrophosph
33	42.5	30.6	569	2	hypothetical prote
34	42.5	30.6	569	2	hypothetical prote
35	42.5	30.6	569	2	hypothetical prote
36	42.5	30.6	569	2	hypothetical prote
37	42.5	30.6	569	2	hypothetical prote
38	42.5	30.6	569	2	hypothetical prote
39	42.5	30.6	569	2	hypothetical prote
40	42.5	30.6	569	2	hypothetical prote
41	42.5	30.6	569	2	hypothetical prote
42	42.5	30.6	569	2	hypothetical prote
43	42.5	30.6	569	2	hypothetical prote
44	42.5	30.6	569	2	hypothetical prote
45	42.5	30.6	569	2	hypothetical prote

ALIGNMENTS

RESULT 1
A:Accession: A36337
C:Date: 12-Apr-1991 *sequence, revision 12-Apr-1991 *text, change 28-Jul-2000
R:HLI, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MIMD:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIS>
A:Cross-references: GB:M57230; NID:g186353; PTDN:AA59155.1; PTD:g186354
A:Gene: GDB:11657; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 100.0%; Score 139; DB 2; Length 918;
Best local similarity 100.0%; Pred. No. 1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 157 NEFLKSEMAHFKADCKAKRDPIS 181

QY 1 NEFLKSEMAHFKADCKAKRDPIS 25

RESULT 2
A:Accession: A36337
C:Date: 02-Aug-1996 *sequence, revision 02-Aug-1996 *text, change 28-Jul-2000
R:HLI, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130.
A:Reference number: 148370; MIMD:9229132
A:Accession: 149699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:g193591; PTDN:AA37723.1; PTD:g193592
A:Accession: 148370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>

```

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817
C:Geneles:
A:gene: gp130
C:superfamily: cytokine receptor homology
C:keywords: glycoprotein
F:134-314/domain: cytokine receptor homology <CR>

Query Match      63.3%; Score 88; DB 2; Length 917;
Best Local Similarity 68.2%; Pred. No. 1e-05;
Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NFPLKSEWATHRFADCKARDT 22
|||||.....|..|||
Db 157 NFPLKSEWATEKFPDCKSKRT 178

RESULT 3
A44257
Interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
A:Reference number: A44257; MID:J9305397
A:Accession: A44257
A>Status: preliminary; not compared with conceptual translation
A:Status: type unknown
A:Position: 1-918 <NN>
A:Experimental source: Liver
A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: cytokine; transmembrane protein
F:134-315/domain: cytokine receptor homology <CR>

Query Match      63.3%; Score 88; DB 2; Length 918;
Best Local Similarity 68.2%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NFPLKSEWATHRFADCKARDT 22
|||||.....|..|||
Db 157 NFPLKSEWATEKFPDCKSKRT 178

RESULT 4
LY9G - mouse
I49059
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 19-May-2000
C:Accession: I49059
R:Kong, S.; Freeman, J.D.; Kelleher, C.; Wager, D.; Takel, F.
J. Immunol. 157, 1417-1423, 1997
A:Title: The Ly9G gene encodes a novel member of a superfamily of type II membrane proteins
A:Accession: I49059
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule: mRNA
A:Residues: 1-266 <RS>
C:Cross-references: EMBL:U01035; NID:9500645; PIDN:AA19053.1; PID:9500646
C:Superfamily: natural killer cell receptor PI-C-type lectin homology

Query Match      36.0%; Score 50; DB 2; Length 266;
Best Local Similarity 40.9%; Pred. No. 2.7;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 NFPLKSEWATHRFADCKARDT 22
|||||.....|..|||
Db 94 DNFLKEMLTINKSDCPSPNE 115

```

```

RESULT 5
T08437
A:Species: Drosophila melanogaster
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Nov-2000
R:Manfield, E. Hershberger, E., Biggs, J., Sherrin, A.
Dev. Biol. 165, 507-526, 1994.
A:Title: Genetic and molecular analysis of hyperplastic discs, a gene whose product 1
A:Accession: T08437
A:Reference number: Z16419; MIMD:59046871
A:Status: preliminary; translated from GR/EMBL/DDBU
A:Feature type: mRNA
A:Features: 1286 <SNP>
A:References: EMBL:U1644; NID:q2673886; PID:q2673887
A:Genetics:
A:Cross-references: Flybase:Pgno000431

Query Match 35.3%; Score 49; DB 2; Length 2895;
Best Local Similarity 60.0%; Prid. No. 43;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 11 HKFADCKAKKDRPTS 25
||| ||| ||| |||
Db 1249 HKHGDCKLKTAPTA 1263

RESULT 6
T27066
A:Protein: hypothetical protein Y51A2B.6a - Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T27066
R:McMurray, A.
Submitted to the EMBL Data Library, January 1998
A:Reference number: Z20305
A:Accession: T27066
A:Status: preliminary; translated from GR/EMBL/DDBU
A:Feature type: mRNA
A:Features: 1717 <SNP>
A:Cross-references: EMBL:M021493; PID:NCA16394.1; GSPDB:GN00023; CESP:Y51A2B.6a
A:Experimental source: clone Y51A2B
C:Genetics:
A:Gene: CESP:Y51A2B.6a
A:Map position: 5
A:Intons: 8/1; 33/1
C:Superfamily: Caenorhabditis elegans hypothetical protein Y10A6C.33

Query Match 33.5%; Score 46.5; DB 2; Length 717;
Best Local Similarity 50.0%; Prid. No. 26;
Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

OY 4 LKSEWATHKFADCKAKKDRPTS 25
||| ||| ||| ||| |||
Db 605 LKSNQMDGR-ADMSLEATWTS 625

RESULT 7
T27067
A:Protein: hypothetical protein Y51A2B.6b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T27067
R:McMurray, A.
Submitted to the EMBL Data Library, January 1998
A:Reference number: Z20305
A:Accession: T27067
A:Status: preliminary; translated from GR/EMBL/DDBU
A:Feature type: DNA
A:Residues: 1-717 <IND>

```

A:Cross-References: EMBL:AL021493; PTDN:CAA16395.1; GSPDB:GN00023; CESP:Y51A2B.6b
 A:Experimental source: clone Y51A2B
 C:Genetics:
 A:Gene: CESP:Y51A2B.6b
 A:Map position: 3
 A:Introns: 6/11; 13/31
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33

Query Match 33.1%; Score 46.5; DB 2; Length 717;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
 Oy 4 LKRSKATKRFADCKAKRPT 25
 Db 605 LKSGCMCHK-ADMSLEMTMTS 625

RESULT 8
 Hypothetical protein s110837 - Synchocystis sp. (strain PCC 6803)
 A:Accession: S110837
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
 C:Accession: S174853
 R:Kanehiko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Matsubae, A.; Yamada, M.; Yasuda DNA Res. 3: 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
 A:Reference number: S174822; M01D:97061201
 A:Accession: S174853
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <KAN>
 A:Cross-References: EMBL:D90909; GB:AB001339; NID:g1652844; PTDN:BM17814.1; PID:d101854
 C:Species: Synchocystis sp.
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
 C:Superfamily: Unassigned tetraatricopeptide repeat (ctrip) tetraatricopeptide repeat
 F:117-150/Domain: tetraatricopeptide repeat homology <TRI>
 F:151-184/Domain: tetraatricopeptide repeat homology <TRI>
 F:185-218/Domain: tetraatricopeptide repeat homology <TRI>
 F:219-252/Domain: tetraatricopeptide repeat homology <TRI>

Query Match 33.1%; Score 46; DB 2; Length 294;
 Best Local Similarity 41.7%; Pred. No. 13;
 Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 NFKLSKATKRFADCKAKRPT 24
 Db 256 DFLVKNLMGEBLIDVTKALFAPPT 279

RESULT 9
 T15253
 Hypothetical protein K07B1.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Accession: T15253
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid K07B1.
 A:Reference number: Z18317
 A:Accession: T15253
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 313 <CAN>
 A:Cross-References: EMBL:AF003384; NID:g208817; PID:g2088621; PTDN:AA54239.1; GSPDB:GN
 C:Genetics:
 A:Gene: CESP:K07B1.3
 A:Map position: 5
 A:Introns: 81/1; 131/3; 236/3; 279/2

C:Superfamily: ADP-ATP carrier protein; ADP-ATP carrier protein repeat homology

Query Match 33.1%; Score 46; DB 2; Length 343;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 NFKLSKATKRFADCKA 18
 Db 232 NFKLKMVLTAVASACA 249

RESULT 10
 S13392.1 - arabinofuranosylase (EC 3.2.1.55) - Pseudomonas fluorescens subsp. cellulosa
 N:Alternate names: xylanase C
 C:Species: Pseudomonas fluorescens subsp. cellulosa
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
 R:Kielietz, L.E.; Poole, D.M.; Ferreira, L.M.A.; Burran, A.V.; Hazlewood, G.P.; Gilbe
 Blockem, J.; 272; 369-376, 1990
 A:Reference number: S13392; M01D:91097447
 A:Accession: S13392
 A:Molecule type: DNA
 A:Residues: 1-571 <REL>
 A:Cross-References: EMBL:X54523; NID:g45523; PTDN:CAA8390.1; PID:g45525
 C:Genetics:
 A:Superfamily: bacterial cellulase-binding domain homology
 C:Keywords: glycosylase; hydrolase
 F:8-134/Domain: bacterial cellulase-binding domain homology <BCB>
 F:39-133/Disulfide bonds: #status predicted

Query Match 33.1%; Score 46; DB 2; Length 571;
 Best Local Similarity 42.9%; Pred. No. 25;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 PTKSPKATKRFADCKAKRPT 22
 Db 41 YTIIDSMSTGFTANITLKNPT 61

RESULT 11
 S16781
 esterase D - Pseudomonas fluorescens
 C:Species: Pseudomonas fluorescens
 C:Date: 22-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
 C:Accession: S16781
 R:Perreira, L.M.A.; Wood, T.M.; Williamson, G.; Pauls, C.; Hazlewood, G.P.; Black, G
 Blockem, J.; 234; 193-224, 1993
 A:Reference number: S16781; M01D:93384502
 A:Accession: S16781
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-583 <PER>
 A:Cross-References: EMBL:X6956; NID:g31110; PTDN:CAA11727.1; PID:g31111
 F:37-113/Domain: bacterial cellulase-binding domain homology <BCB>

Query Match 33.1%; Score 46; DB 2; Length 583;
 Best Local Similarity 42.9%; Pred. No. 26;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 PTKSPKATKRFADCKAKRPT 22
 Db 40 YTIIDSMSTGFTANITLKNPT 60

RESULT 12

SI1391
 Enolase 1,4-beta-xylanase (EC 3.2.1.8) B - Pseudomonas fluorescens subsp. cellulosa
 C:Accession: F1391
 C:Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999
 R:Kelllett, L.E.; Poole, D.W.; Ferreira, L.M.A.; Duranti, A.J.; Hazlewood, G.P.; Gilbert,
 Blochman, J. 272, 369-376, 1990
 A:Title: Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. cellu
 A:Accession: SI1391, M01D:9109/447
 A:Molecule type: DNA
 A:Residues: 1-592 <EMBL>
 A:Cross-references: EMBL:X54523; NID:945523; PIDD:CAA38389.1; PID:945524
 C:Genetics:
 A:Gene: xynB
 C:Function:
 A:Enzymatic: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
 A:Pathway: xylan degradation
 C:Superfamily: Pseudomonas endo-1,4-beta-xylanase B; bacterial cellulose-binding domain
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:38-133/Domain: bacterial cellulose-binding domain homology <CB>
 F:337-592/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SX>
 F:337-133/Disulfide bonds: #status predicted
 F:431,530/Active site: Glu #status predicted

Query Match 33.1%; Score 46; DB 1; Length 592;
 Best Local Similarity 42.9%; Pred. No. 26;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 FTLSSEMTAFKADCKAKRDT 22
 DB 41 YTHSSSTGTFAMTLTKNDT 61

RESULT 13
 EBI337
 Probable nonribosomal peptide synthetase PA4078 [Imported] - Pseudomonas aeruginosa (str
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 R:Stover, C.K.; Pham, X.O.; Eryilm, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; Bz
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardijs, K.; Llm,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
 A:Accession: F1391, M01D:9109/447
 A:Reference number: M01D:20437357
 A:Cross-references: EMBL:X54523; GB:AB004091; NID:99950265; PIDD:AA007465.1; GSPDB:GN001
 A:Residues: 1-991 <STO>
 A:Molecule type: DNA
 A:Status: preliminary
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: PA4078
 C:Enzymatic: 1,4-epi carrier protein homology; acetate--CoA ligase homology
 C:Keywords: carrier protein
 F:507-488/Domain: acetate--CoA ligase homology <AC>
 F:507-575/Domain: acyl carrier protein homology <ACP>

Query Match 33.1%; Score 46; DB 2; Length 991;
 Best Local Similarity 40.0%; Pred. No. 43;
 Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 4 LKSEMTAFKADCKAKRDT 23
 DB 790 VRSKWKEITADIAERGLP 809

RESULT 14
 T16403

hypothetical protein F17C15.180 - Arabidopsis thaliana
 C:Accession: F17C15.180
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 R:Bayvan, M.; Pohl, T.; Weizenecker, T.; Baneroff, I.; Mewes, H.W.; Rudd, S.; Lemcke,
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224492
 A:Accession: 748403
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-533 <EB>
 A:Cross-references: EMBL:A162506
 A:Experimental source: cultivar Columbia; BAC clone F17C15

A:Map position: 5 110/3; 143/3; 265/1; 310/3; 348/3; 415/2; 480/2
 A:Note: F17C15.180

Query Match 32.7%; Score 45.5; DB 2; Length 533;
 Best Local Similarity 52.4%; Pred. No. 28;
 Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 6 SEMATFHKADCKAKRDT 25
 DB 449 NEMVTEKSDVKNKSNKTS 469

RESULT 15
 P10186
 Ig lambda chain, C region - sandbar shark (fragment)
 C:Species: Carcharias plumbeus (sandbar shark)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Nov-2000
 R:Schubert, S.F.; Beischel, C.J.; Martin, S.A.; Marchionis, J.J.
 Mol. Immunol. 27, 17-23, 1990
 A:Title: Sequence analysis of homogeneous peptides of shark immunoglobulin light chain
 A:Reference number: P10186; M01D:90190677
 A:Cross-references: EMBL:X54523; GB:AB004091; NID:99950265; PIDD:AA007465.1; GSPDB:GN001
 A:Residues: 1-991 <STO>
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Experimental source: serum
 C:Genetics:
 A:Gene: SHLC6
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 32.4%; Score 45; DB 2; Length 67;
 Best Local Similarity 41.2%; Pred. No. 4.2;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 6 SEMATFHKADCKAKRDT 22
 DB 36 SEMSNELTSCVKNHT 52

Search completed: December 19, 2001, 16:22:40
 Job time: 460 sec

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CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC DISSEMIN: GP130 RAPS IS AN OUTGROUP TO PRINTS WITH RA
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide cd30 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/pubmed/cd30.htm"
 CC
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 CC
 CC EMBL: M57230; AA50155.1; -
 CC EMBL: AB015706; BA078112.1; -
 CC PIR: A36337; A36337.
 CC PDB: 1BOU; 26-AUG-98.
 CC MIM: 600694; -
 CC InterPro: IPR002996; CRA.
 CC InterPro: IPR003572; FN.LIT.
 CC Pfam: PF00041; fn3; 3
 CC PRINTS: PR00014; FNTEP111.
 CC SMART: SM00060; FN3; 3.
 CC PROSITE: PS01353; HEMATOPO.REC.L.F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat: 30-structure; Alternative splicing.
 CC
 CC CHAIN 23 918
 CC DOMAIN 23 619 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC TRANSMEM 620 918 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 642 918 POTENTIAL.
 CC DOMAIN 126 120 CYTOLASMIC (POTENTIAL).
 CC DOMAIN 124 222 I6-LIKE C2-TYPE DOMAIN.
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 CC DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
 CC DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
 CC DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
 CC DOMAIN 725 755 FIBRONECTIN TYPE-III 5.
 CC
 CC DISULFID 28 54
 CC DISULFID 48 103
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 CC DISULFID 458 466
 CC CARBOHYD 43 43
 CC CARBOHYD 83 83
 CC CARBOHYD 131 131
 CC CARBOHYD 137 157
 CC CARBOHYD 227 227
 CC CARBOHYD 359 383
 CC CARBOHYD 553 553
 CC CARBOHYD 554 564
 CC CARBOHYD 335 329
 CC VARSPLIC 330 918
 CC
 CC SEQUENCE 918 AA: 103522 MW: D81363672D01D053 CRC64;
 CC
 CC Query Match 100.0%; Score 139; DB 1; Length 918;
 CC Best Local Similarity 100.0%; Pred. 2.8e-14;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 NFKLSEMTATKRFADCKAKKRDPTPS 161
 DB 157 NFKLSEMTATKRFADCKAKKRDPTPS 161
 RESULT 2

IL6B_MOUSE STANDARD: PRT: 917 AA.
 AC 000560
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (I6-66-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER (MEMBRANE GLYCOPROTEIN 130) (GP130).
 DE
 DE LUS1; Musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STAIN-FOR TISSUE=Macrophages;
 RX Seto M, Yoshida K, Hibi M, Tera T., Kishimoto T.;
 RE Molecular cloning of a murine IL-6 receptor-associated signal
 RE transducer, gp130, and its regulated expression in vivo.*
 RL J. Immunol. 148:4056-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, ILF, OSM, CTRF, AND IL-11 CAN UTILIZE GP130 AS A SHARED
 CC RECEPTOR IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THYMUS.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS SPLEEN, THYMUS,
 CC EXCEPT BAF-B01. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CC CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 CC DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL: X62646; CAA44515.1; -
 CC DR HSSP: M83136; AA37723.1; -
 CC DR HSSP: P40189; 1BOU.
 CC DR MGD: MG1:96560; 1166t.
 CC InterPro: IPR002996; CRA.
 CC InterPro: IPR003572; FN.LIT.
 CC Pfam: PF00041; fn3; 4
 CC PRINTS: PR00014; FNTEP111.
 CC SMART: SM00060; FN3; 2.
 CC PROSITE: PS01353; HEMATOPO.REC.L.F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat:
 CC CHAIN 23 917
 CC DOMAIN 23 617 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC TRANSMEM 618 917 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 640 917 POTENTIAL.
 CC DOMAIN 126 120 CYTOLASMIC (POTENTIAL).
 CC DOMAIN 124 222 I6-LIKE C2-TYPE DOMAIN.
 CC DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 221 322 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 422 515 FIBRONECTIN TYPE-III 3.
 CC DOMAIN 516 611 FIBRONECTIN TYPE-III 4.
 CC DOMAIN 723 741 FIBRONECTIN TYPE-III 5.
 CC
 CC SRR-RICH.

RN	(1)	
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 39-56.	
RN	STRAIN=SP. CELLULOZA. PWD62128205.	
RA	Kellert L.E., Poolle D.M., Ferreira L.M.A.V., Durant A.J.,	
RA	Hazelwood G.P., Gilbert H.J.,	
RT	Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens	
RT	susp.: cellulosa contain identical cellulose-binding domains and are	
RT	nubsp. by adjacent genes' .	
RL	Biochim J. 272:369-376(1990).	
CX	- FUNCTION: XYLANASE IS ANOXYGEN-BINDING TO HYDROLIZE HELMICELLOSE, THE	
CX	CELLULOSE POLYMER WITH A MOLECULAR WEIGHT OF UP TO 10 ⁶ .	
CX	- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING ALPHA-L-	
CX	ARABINOFURANOSE RESIDUES IN ALPHA-L-ARABINOSES.	
CX	- PATHWAY: HELMICELLOUSE DEGRADATION.	
CX	- SUBCELLULAR LOCATION: SECRETED.	
CX	- MISCELLANEOUS: ACTS ONLY ON HIGH MW SUBSTRATES, IN WHICH ARABINOSE	
CX	IS LINKED TO A POLYMERIC BACKBONE.	
CX	- SIMILARITY: CONTAINS I BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN	
CX	- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.	
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CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed, usage by and for commercial	
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ license.html#db) (http://www.isb-sib.ch/announcement/)	
CC	EMBL; X54523; CAH38390.1; .	
DR	PTR: S13392; S13392.	
DR	HSSP: P01088; 1BPV.	
DR	IInterpro: IPROU01919; CBD_2.	
DR	IInterPro: PROU01899; Gran_Pos_anchor.	
DR	PSORT: PSOU0561; Cbd_BactGAL_1.	
FT	Hydrolase; Glycosidease; Signal.	
FT	SIGNAL 1 38	
FT	CHAIN 39 571 ALPHA-L-A-RABI-N-O-FURANOSI-DASE C.	
FT	DOMAIN 39 114 CELLULOSE-BINDING (BY SIMILARTY).	
FT	DOMAIN 135 160 SER-RICH (LINKER).	
FT	DOMAIN 300 330 SER-RICH (LINKER).	
FT	DOMAIN 330 571 BD_555	
FT	FUNCTION 571 AA; 61072 MW; AD19585PEBD555 CRC64;	
SO	SEQUENCE	
Oy	Query Match 33.1%; Score 46; DB 1; Length 571; Best Local Similarity 42.9%; Pred. No. 9.8; Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;	
Nb	41 YTTDSNSTGTGPANTLKNT 61	
RESULT 8		
XTNB_YERNL	STANDARD; PRF: 592 AA.	
AD	EPI3030	
DT	01-NOV-1991 (Rel. 20. Created) 01-NOV-1991 (Rel. 20. Last sequence update) 15-JUL-1999 (Rel. 38. Last annotation update) DE	MOD-1,4-BETA-XYLANASE B PRECURSOR [EC 3.2.1.8] (XYLANASE B)
GN	XYLN.	
GNS	Pseudomonas fluorescens	
OC	Familia: Proteobacteria, gamma subdivision: Pseudomonadaceae:	
OC	Pseudomona	
NCBI_TaxId=294;		
OX	(1)	
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 39-56. C STRAIN=SP. CELLULOZA.	

```

RX MEDLINE:9109/447. PubMed:2123205.
RA Releith L.E., Poole D.N., Ferreira L.M.A., Durrant A.J.,
RA Hazledorn G.B., Gilibert I. Cellulose-degrading enzymes from Pseudomonas fluorescens
RA strain 10000: a family of cellulose-binding domains and a family of cellulose-binding
RA subp. cellulosa contain identical cellulose-binding domains and are
RT encoded by adjacent genes.
RT Biochem J. 272:369-376(1990).
CC - FUNCTION: XYLANASE B CATALYZES TO HYDROLYSE HEMICELLULOSE, THE
CC MAJOR COMPONENT OF PLANT CELL-WALLS.
CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC GLUCOSIDES TO GLUCOSE AND XYLULOSE BY HYDROLYTIC DEGRADATION.
CC - SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
CC - SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CDB).
CC
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CC
DR EMBL: X34523; CAA38389.1; -.
DR PIR: S13581; S13591.
DR DDB: J02868; J02869.
DR InterPro: IPR001319; Glyco_2
DR InterPro: IPR001000; Glyco_hydro_10.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00553; CBD_2; 1.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR PRINTS: PR00134; GLHDBLASL0.
DR PROSITE: PS00551; GLYCOSYL_HYDROL_F10; 1.
DR SMART: SM00486; GLYCOSYL_HYDROL_F10; 1.
DR KEGG: K02868; K02869.
DR Cellulose degradation; Xylan degradation; Hydrolyase; Glycosidase;
KW signal.
FT FT SIGNAL 1 38
FT CHAIN 39 592 ENDO-1,4-BETA-XYLANASE B.
FT FT DOMAIN 39 134 CELLULOSE-BINDING (BY SIMILARITY).
FT FT DOMAIN 135 160 SER-RICH (LINKER).
FT FT DOMAIN 161 200 SER-RICH (LINKER).
FT FT DOMAIN 201 300 SENSITIVE TO HYDROLYTIC DEGRADATION (BY SIMILARITY).
FT FT DOMAIN 301 420 SENSITIVE TO HYDROLYTIC DEGRADATION (BY SIMILARITY).
FT FT ACT_SITE 530 530 NUCLEOPHILE (BY SIMILARITY).
FT FT DISULFID 39 133 BY SIMILARITY.
SQ SEQUENCE 592 AA: 63410 MW: 63410 MW: E081E630E8A2B93A CRC64;

Query Match 33.18; Score 46; DB 1; Length 592;
Evalue 1e-108; Identities 10; Mismatches 0;
Matches 9; Conservative 4;
Db 2 PFKLSNATKRNKACKAKARPT 22
1:||||:1:1:11
Db 41 YTDSMSTGFANITMLNDT 61

RESUME 9
ID KLR8_MOUSE STANDARD; PRT: 266 AA.
AC 060682; 078027.
DT 01-NOV-1997 (Re1. 35, Created)
DT 01-NOV-1997 (Re1. 35, Last sequence update)
DT 20-AUG-2001 (Re1. 40, Last annotation update)
DE KILLER CELL DECTIN-LIKE RECEPTOR 8 (T-CELL SURFACE GLYCOPROTEIN
DE KLR8) OR LY49H OR LY49H-H.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Canalia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NC NCBI_TaxID:10090;
LN
LN [1]

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ET	STRAND	348	353
ET	STRAND	362	362
ET	HELI	364	366
ET	STRAND	367	367
ET	STRAND	370	370
ET	TORN	384	385
ET	STRAND	390	406
ET	TORN	423	426
ET	TORN	431	431
ET	TORN	431	431
ET	STRAND	438	438
ET	STRAND	444	445
ET	TORN	449	450
ET	STRAND	457	457
ET	STRAND	457	457
ET	HELI	458	463
ET	STRAND	466	467
ET	STRAND	470	471
ET	TORN	473	474
ET	STRAND	477	478
ET	STRAND	480	483
ET	TORN	489	500
ET	TORN	499	506
ET	TORN	503	506
ET	HELI	508	513
ET	HELI	514	515
ET	TORN	516	520
ET	STRAND	523	529
ET	STRAND	532	534
ET	TORN	534	534
ET	HELI	544	557
ET	TORN	558	559
ET	TORN	561	566
ET	STRAND	572	577
ET	STRAND	586	587
ET	STRAND	601	611
ET	TORN	614	615
ET	STRAND	616	616
ET	TORN	631	631
ET	STRAND	633	637
ET	STRAND	648	651
ET	HELI	651	653
ET	TORN	661	664
ET	TORN	676	677
ET	STRAND	678	678
ET	HELI	683	687
ET	TORN	696	699
ET	STRAND	706	707
ET	TORN	708	709
ET	TORN	710	711
ET	STRAND	721	725
ET	STRAND	721	722
ET	TORN	727	733
ET	TORN	737	738
ET	STRAND	741	741
ET	STRAND	744	744
ET	STRAND	752	752
ET	STRAND	755	755
ET	HELI	758	762
ET	STRAND	762	763
ET	STRAND	766	779
ET	STRAND	794	795
ET	TORN	806	807
ET	TORN	810	812
ET	HELI	818	822
ET	STRAND	828	833
ET	STRAND	842	843
ET	STRAND	847	847
ET	STRAND	849	849
ET	TORN	853	854

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query	5 KSEBATEKREDOCKARNDP 22	Matches	Conservative	Indels	Gaps
Db	1681 EETWAKREKDYRIEHD 1698	4;	7;	0;	0;

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity	Score	DB 1:	Length	2301:
Matches 7; Conservative	30.9%	43;	DB 1:	Length 2301:	
Indels 0;					
Gaps 0;					

Query Match	Best Local Similarity</
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SQL SEQUENCE 569 AA; 64235 MM; 5118042478DF00FC CRC64;

Query Match 30.6%; Score 42.5; DB 1; Length 569;

Best Local Similarity 52.4%; Pctid No 35;

Matches 11; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

0Y 5 KSEWATEKFAADCKA-KRDFT 24

DB 329 KQKATHOLAPCRKMLRDYDT 349

Search completed: December 19, 2001, 16:26:18
Job time: 573 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:24 ; Search time 157.32 Seconds
(without alignments)
23.244 Million cell updates/sec

Title: US-09-202-104a-8

Sequence: 1 NFKLSEWATHKAFADCKAKKRDPTPS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries
SPRBRML.17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.plant:*
7: sp.phage:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.protein:*
12: sp.virus:*
13: sp.verticillate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	329	4 Q9U041	Q9U041 homo sapien
2	50	36.0	361	2 Q9CBN2	Q9CBN2 mycobacteri
3	50	36.0	2798	4 Q9NFI3	Q9NFI3 homo sapien
4	48	35.3	266	11 Q61198	Q61198 mus muscu
5	48	35.3	2193	12 Q9YF63	Q9YF63 mus muscu
6	48	34.5	131	9 Q9A443	Q9A443 mus muscu
7	48	34.5	131	9 Q9A443	Q9A443 mus muscu
8	48	34.5	131	9 Q9A443	Q9A443 mus muscu
9	48	34.5	530	5 Q9VJ55	Q9VJ55 drosophila
10	48	34.5	1456	5 Q9W3M2	Q9W3M2 mus muscu
11	47	33.8	60	11 Q88362	Q88362 mus muscu
12	47	33.8	60	11 Q88362	Q88362 mus muscu
13	46.5	33.8	717	5 Q45559	Q45559 fowl adeno
14	46.5	33.1	196	12 Q55275	Q55275 fowl adeno
15	46	33.1	294	2 P73762	P73762 synectocyst
16	46	33.1	343	5 Q01883	Q01883 caenorhabd
17	46	33.1	565	2 Q9W501	Q9W501 plasmu salli
18	46	33.1	583	2 Q51815	Q51815 pseudomonas

20	46	33.1	751	11 Q99MK1	Q99MK1 mus muscu
21	46	33.1	778	11 Q99MK1	Q99MK1 mus muscu
22	46	33.1	830	12 Q8363	Q8363 alleparvata
23	46	33.1	887	5 Q9VAG1	Q9VAG1 drosophila
24	45.5	33.1	533	10 Q91ZP3	Q91ZP3 mus muscu
25	45	32.4	59	11 Q88360	Q88360 mus muscu
26	45	32.4	59	11 Q88360	Q88360 mus muscu
27	45	32.4	266	11 Q9A106	Q9A106 mus muscu
28	45	32.4	266	11 Q9A106	Q9A106 mus muscu
29	45	32.4	266	11 Q9A106	Q9A106 mus muscu
30	45	32.4	266	10 Q9S214	Q9S214 aradidopsis
31	45	32.4	289	10 Q38810	Q38810 aradidopsis
32	45	32.4	381	5 Q18873	Q18873 mus muscu
33	45	32.4	552	5 P91765	P91765 myzus persi
34	45	32.4	552	5 P91765	P91765 myzus persi
35	44.5	32.0	331	10 Q9S060	Q9S060 oryza sativ
36	44.5	32.0	331	10 Q9S060	Q9S060 oryza sativ
37	44.5	32.0	994	4 Q9Y489	Q9Y489 homo sapien
38	44.5	32.0	1003	2 Q9AHF2	Q9AHF2 arcanobacte
39	44.5	32.0	1557	5 Q9XKC3	Q9XKC3 caenorhabd
40	44.5	31.7	214	5 Q9N8A4	Q9N8A4 leishmania
41	44	31.7	263	7 Q78027	Q78027 mus muscu
42	44	31.7	263	7 Q78027	Q78027 mus muscu
43	44	31.7	266	11 Q9JHV1	Q9JHV1 mus muscu
44	44	31.7	362	2 Q9EW70	Q9EW70 streptomyce
45	44	31.7	957	5 Q9GVY4	Q9GVY4 drosophila

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	329 AA.
ID Q9U041	Q9U041		
AC Q9U041	Q9U041		
AT Q9U041	Q9U041		
DT 01-MAY-2000 (TREMBL 13, Created)			
DE 01-JUN-2001 (TREMBL 17, Last annotation update)			
DE GP130 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE			
DE FORM (GP130-RAFS).			
GN GP130.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.			
NC MGI:145606			
LN [1]			
RP TSSUPE-SYNONYM;			
RP SEQUENCE FROM N.A.			
RA Tanaka M., Kishimura M., Ozaki S., Hashimoto H., Osaka F., Okubo M.,			
RT "Cloning of novel soluble gp130 and detection of its neutralizing			
RT antibody using human monoclonal antibody to the gp130/CD136			
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
DR EMBL: AB015706; BAW7812.1; .			
DR HSP: P40189; IBDU.			
DR InterPro: IPR002956; CRA1.			
DR InterPro: IPR003962; PA1L1; Repeat.			
DR InterPro: IPR003961; FN_111.			
DR Pfam: PF00041; fn3; Ig-like fold.			
DR SMART: SM00060; fn3; 1.			
KW Repeat.			
SQ			
SEQUENCE 329 AA: 37484 MW; D976576B34FC596 CRC64;			
Query Match	100.0%	Score 139	DB 4;
Best Local Similarity	100.0%	Field No. 5	Le-15;
Matches 25;	Conservative 0;	Mismatches 0;	Indels 0;
Gapes 0;			
QY 1 NFKLSEWATHKAFADCKAKKRDPTPS 25			
DB 157 NFKLSEWATHKAFADCKAKKRDPTPS 181			

OS	Squash leaf curl virus.		
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.		
OX	NCBI_TaxID=10829;		
RN	1)		
RL	SEQUENCE FROM N.A.		
RA	SPRINT-LOS MCHSIS L1		
RB	Londale A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;		
RC	Submitted (JAN-1994) to the EMBL/Genbank/DDJJ databases.		
DR	EMBL; J27272; AAA4819.1;		
DT	InterPro: IPR001191; GeneM_Atl.		
DZ	Pfam: PF00739; GeneM_Atl; 1.		
DR	ProDom: PD00736; GeneM_Atl; 1.		
FT	NON_TER		
FI	93		
FJ	93		
SQ	SEQUENCE 93 AA; 10550 MW; 35CDH3B8C5D0765D CRC64;		
Query Match	34.5%; Score 48; DB 12; Length 93;		
Best Local Similarity	50.0%; Pred.No. 1.7;		
Matches	9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;		
CY	8 WATHKEDCKAKADPTPS 25 :		
Db	71 WADDFECGSAARPPRS 88		
RESULT 7			
Q9NAZ2 Q9NAZ2 PRELMINARY; PRT; 131 AA.			
AC AC			
DD	01-JUN-2001 (TREMBLrel_17_Created)		
DT	01-JUN-2001 (TREMBLrel_17_Last sequence update)		
DT	01-JUN-2001 (TREMBLrel_17_Last annotation update)		
DE	COAT PROTEIN.		
OS	Bacteriophage AP205.		
OC	Viruses; ssRNA positive-strand viruses; no DNA stage; Leviviridae;		
OX	NCBI_TaxID=154784;		
RN	1)		
RL	SEQUENCE FROM N.A.		
RA	Klovins J., Overbeek G.P., Ackermann H.W., Van Duin J.;		
RB	"Nucleotide sequence of a single-stranded RNA phage from		
RC	Actinobacterium: an unusual genetic map."		
DR	Submitted (JAN-2001) to the EMBL/Genbank/DDJJ databases.		
DT	EMBL; J3111; AAA2033.1;		
DL	SEQUENCE 131 AA; 14009 MW; FBKECBGB8E12952 CRC64;		
Query Match	34.5%; Score 48; DB 9; Length 131;		
Best Local Similarity	80.0%; Pred.No. 2.5;		
Matches	8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
CY	3 TLASEMTKH 12 		
Db	92 TLASEMTKH 101		
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ID Q9NJ16 PRELMINARY; PRT; 416 AA.			
DD	01-OCT-2000 (PRELMINrel_15_Created)		
DT	01-OCT-2000 (TREMBLrel_15_Last sequence update)		
DT	01-OCT-2000 (TREMBLrel_15_Last annotation update)		
DE	HYPOTHETICAL PROTEIN Y49F6A.5.		
GN	y49f6a.5		
OC	Cenothaditis elegans.		
OC	Eukaryota; Metazoa; Nematoea; Chromodorea; Rhabditiida; Rhabditoleae;		
OX	Nematoidea; Ctenophoridae; Cenothaditidae;		
OX	NR01_Txalid=9239;		
RN	1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BESTOL NZ;		

RA	MEDLINE-990656313; PubMed-5851916; None;
RA	"Genome sequence of the nematode <i>C. elegans</i> : a platform for
RT	reverse genetics."
RT	Science 283:2012-2016(1998).
RN	[2]
RA	SEQUENCE FROM N.A.
RA	STRAIN-BRISTOL N2.
RA	Miller N., La T.
RT	"The sequence of <i>C. elegans</i> cosmid v49p6a."
RT	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RA	SEQUENCE FROM N.A.
RA	STRAIN-BRISTOL N2.
RA	Waterston R.;
RA	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RA	EMBL: AC024800; AF50726.1; -
DR	SEQUENCE 416 AA; 48245 MW; 46424C24BBA8738 CRC64;
Qy	4 LKSEWATEKADCKAKKADPT 24
Db	12 VKRNMDDHMTSSCATSPSP 32
Qy	1 2 3 4 5 6 7 8 9 10 11 12
Db	1 2 3 4 5 6 7 8 9 10 11 12
RESULT	9
Qy	09VJ55 PRELIMINARY; PRT; 530 AA.
ID	09VJ55
DT	01-MAY-2000 (TRENBLURE). 13, Created
DT	01-MAY-2000 (TRENBLURE). 13, Last sequence update
DE	CG10346 PROTEIN.
DE	CG10346 PROTEIN.
GN	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha
OC	Ephyridia; Drosophilidae; Drosophila.
OC	NCBI_TaxID=7227;
RA	SEQUENCE FROM N.A.
RA	STRAIN-BRELEAY.
RA	MEDLINE-20196006; PubMed-10731132;
RA	Adams M.D., Gelliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Angelidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Stetson G.C., Wortman V.R., Chang F., Delrow M.D., Zhang J., Chen Liffer B.D.,
RA	Man K.H., Doyle J.C., Baxter E.C., Fung H.C., Gabor C.R., Makos G.L.G.,
RA	Abell J.F., Agbayani A., An H.T., Andrews-Pfannkoch C., Baldwin D.,
RA	Balfe R.M., Basu A., Baxendale J., Bayraktoglu D., Belsky E.M.,
RA	Beeson K.Y., Bowen P.V., Beckman B.P., Bhandal D., Bolshakov S.,
RA	Borkov D., Botchan M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Burley K.C., Busan D.A., Butler H., Cadelis E., Genter A., Gilmara I.,
RA	Berry J.M., Cavley S., Dahlke C., Davenport L., Desmet M.,
RA	Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Dubin K.T., Evangelista C.C., Ferraz C., Pettersen S., Fleischmann W
RA	Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J., Houck J.,
RA	Hoskins D., Houston K.A., Howard T.J., Wei M.-H., Deegman K.A.
RA	Jatani M., Kalush F., Karpen G.H., Ke A.E., Kenison J.A., Ketchum K.A.
RA	Laslo P., Leal Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosteffi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Wuzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,

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RA. Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RX. MEDLINE=94150718, Pubmed=7906398;
 RX. REFERENCE FROM N.A.
 RA. 12)
 RA. Wilsen R., Altmough R., Connell K., Baynes C., Berka M.,
 RA. Milford J., Burton J., Connell M., Cossy T., Cooper T., Coulson A.,
 RA. Craxton M., Dear S., Du G., Durbin R., Favello A., Fulton L.,
 RA. Gaudet A., Grosse P., Heston J., Hiles M., Jamieson L.,
 RA. Johnston A., Jones P., Keston J., Keston M., Lattelle P.,
 RA. Lightfoot J., Lloyd C., Mennar A., Mortimore B., O'Callaghan R.,
 RA. Parsons T., Percy C., Rifkin L., Rogers A., Saunders B., Shownkeen R.,
 RA. Smalton R., Smith A., Sommerer E., Staden R., Sulston J.,
 RA. Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RT	aligns % coverage distance from chr6:90780000
RL	Nature 368:32-38(1996)
DR	EMBL; AL021493; C11G03A.1; -
DR	InterPro: IPR003125; MSN.
Pfam:	PF02206; MSN; 1.
DR	SMART; SMO0453; MSN; 1.
QO	SEQUENCE 717 AA; 81.75 MW; EA9C79E40EFBDE CRC64;

Query Match	33.5%;	Score 46.5;	DB 5;	Length 717;
Best Local Similarity	50.0%;	Pred. No. 24;		

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AC	045959										
MC	01-JUN-1998	(TREMURFL_06	Created)								
DT	01-JUN-1998	(TREMURFL_06	Last sequence update)								
DE	Y51A2B.68 PROTEIN.										
GN	Y51A2B.68										
OC	Caenorhabditis elegans.										
OS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdillida; Rhabdilloidea;										
ON	Rhabdillidae; Poliderrinae; Caenorhabditis.										
OR	NBL_TaxID=6239;										
RP	SEQUENCE FROM N.A.										
RT	McMurry A.;										
RL	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.										
RD	[2]										
RA	SEQUENCE FROM N.A.										
RX	MEDLINE=9415018; PubMed=7306398;										
RY	MESH=D013501; MESH=C00013501;										
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SB	Bontfeld J, Albrecht U, Connell M, Cooper J, Cooper J, Garske D, Hargrave S,										
SC	Carlson M., Dear S., Di Z., Duphin R, Pavello A., Fulton L.,										
SD	Garner A., Green P., Hawkins T., Hillier L., Jler M., Johnson L.,										
SE	Jones M., Kersey B., Kirsten J., Laister N., Latreille P.,										
SF	Lighting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan R.,										
SG	Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,										
SH	Stratton N., Smith A., Sonnenhammer E., Steadun R., Stulton J.,										
SI	Talbot W., Threlkeld J., Thomas R., Tomlinson R., Vaughan K., Waterston R.,										
SJ	Watson A., Watson J., Watson J., Watson J., Watson J., Watson J.,										
SK	2 Mb of contiguous nucleotide sequence from chromosome III of C.										
SL	elegans. #;										
SM	Nature 368:32-38(1994).										
SN	EMBL; AL021493; CAI61395.1; *										
SO	InterPro: ITR001325; MSN.										
SR	SWIFT; SWO25; MSN. 1;										
SS	SEQUENCE 717 AA; 8189 MW; 1AE394886B373AB CRC64;										
ST	Query Match	33.5%; Score 46.5; DB 5; Length 717;									
TD	Best Local Similarity	50.0%; Pred. No. 24;									
TE	Matches 11: Conservative	7; Mismatches 7; Indels 1; Gaps 1;									
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TH											
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TR	01-JUN-1998	(TREMURFL_06	Created)								
TS	01-JUN-1998	(TREMURFL_06	Last sequence update)								
TT	01-AUG-1998	(TREMURFL_07;	Last annotation update)								
TU	33K PROTEIN.										
TV	33K.										
TX	Fowl adenovirus.										
TY	VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.										
TA	NBL_TaxID=31540;										
TB	SEQUENCE FROM N.A.										
TC	Johnson M.A., Shepard M., Teates F.;										
TD	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.										
TE	EMBL; AF006739; AB988279.1; *										

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SQ      SEQUENCE      196 AA: 21919 MW: 50819A3FA5DB83 CRC64:
Query Match      33.1%      Score 46; DB 12; Length 196;
Best Local Similarity 33.3%; Pred. no. 8;
Matches 8; Conservative 3; Mismatches 4; Gaps 0;
QY      8 MATHFMDCAKRDT 22
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Db      133 MARYVAICQALRDT 147

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Job time: 551 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:01 : Search time 78.52 seconds
(without alignments)
7.165 Million cell updates/sec

File: us-09-202-104a-8

Protein score: 1 NPTLAKSWMTKFDCAKREPTPS 25

Sequence: BLOSUN62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents, AA:*

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- 2: /cgn2.6/pdata/2/1aa/5a.COMB.pep:*
- 3: /cgn2.6/pdata/2/1aa/6a.COMB.pep:*
- 4: /cgn2.6/pdata/2/1aa/6b.COMB.pep:*
- 5: /cgn2.6/pdata/2/1aa/CTUS.COMB.pep:*
- 6: /cgn2.6/pdata/2/1aa/Backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	139	100.0	488	2 US-08-599-455B-5
2	139	100.0	488	4 US-09-069-781B-5
3	139	100.0	572	2 US-08-419-652-5
4	139	100.0	658	2 US-08-825-558-4
5	139	100.0	708	1 US-07-797-556-2
6	139	100.0	708	1 US-08-368-881-2
7	139	100.0	708	1 US-09-059-059-2
8	139	100.0	708	2 US-09-058-264-2
9	139	100.0	708	5 US-08-925-558-6
10	139	100.0	918	2 US-08-925-558-6
11	139	100.0	918	2 US-08-925-558-6
12	46	33.1	592	1 US-08-217-377-8
13	42.5	30.6	488	4 US-08-910-313-8
14	41	29.2	525	1 US-08-461-599-19
15	41	29.5	525	1 US-08-461-599-19
16	41	29.5	525	1 US-08-461-599-19
17	41	29.5	525	1 US-08-461-599-19
18	41	29.5	525	1 US-08-461-599-19
19	40	28.8	77	4 US-08-803-346-62
20	40	28.8	77	4 US-08-803-346-62
21	40	28.8	171	1 US-07-949-812-7
22	40	28.8	171	1 US-07-949-812-7
23	40	28.8	514	2 US-08-960-025-1
24	40	28.8	894	4 US-08-059-458-2
25	40	28.8	894	4 US-08-059-458-2
26	40	28.8	895	4 US-08-827-962-19
27	40	28.8	895	4 US-08-827-962-21

28	40	28.8	896	2 US-08-640-389A-12
29	40	28.8	1162	2 US-08-599-455B-5
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34	40	28.8	1162	4 US-08-827-962-20
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38	37	28.1	55	1 US-07-862-021B-20
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ALIGNMENTS

RESULT 1
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Targadia, Louis A.
; APPLICANT: Cephalon, Inc.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: GENES 2.0 Windows version 2.0
CURRENT APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; FILING DATE: 27-NOV-1995
; NAME: Melkijohn Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-8906
; TELEFAX: 617-542-8906
; INVENTOR: ID NO. 5:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
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Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
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Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 45, Appl

MOLECULE TYPE: protein
US-08-599-455B-5

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Best Local Similarity 100.0%   Pred. NO, 1.4e-14;
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Db      126 NPTLSEMAHTKPRDCKAKKDDPPS 152

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RESULT 2
 US-09-059-781B-5
 Sequence 5. Application US/09069781B
 Patent No. 6287782
 GENETIC INFORMATION:
 APPLICANT: Gail, Louis A.
 APPLICANT: Toppert, Robert I.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY
 TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS: Richardson, P.C.
 ADDRESS: 225 Franklin Street
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: Windows 95
 SOFTWARE: PatsISO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,781B
 FILING DATE: 29-APRIL-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/864,564
 FILING DATE: 28-MAY-1990
 APPLICATION NUMBER: US 08/706,123
 FILING DATE: 28-APR-1989
 APPLICATION NUMBER: US 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: US 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: US 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: US 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: US 08/565,485
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: US 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: US 08/563,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Melkijohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: U7334/082001
 TELEPHONE/CALL NUMBER: 542-8070
 TELEPHONE: (617) 542-8070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781B-5

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Query Match 100.0% Score 139, DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 NPTLSSPMATHKRFPOCKAKKDPPPS 152

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RESULT 3
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2 Patent No. 56310070N:
3 GENETIC INFORMATION:
4 APPLICANT: Hoffmann-La Roche Inc.
5 APPLICANT: Gubler, Ulrich A
6 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
7 NUMBER OF SEQUENCES: 7
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Hoffmann-La Roche Inc.
10 STREET: 340 Kingsland Street
11 CITY: Nutley
12 STATE: New Jersey
13 COUNTRY: USA
14 ZIP: 07110-1199
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: PC compatible
18 OPERATING SYSTEM: MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 PUBLICATION NUMBER: US/08/419,652
22 FILING DATE: 14APR-1995
23 CLASSIFICATION: 530
24 PRIORITY INFORMATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/248,532
27 FILING DATE: 31-MAY-1994
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/094,713
30 FILING DATE: 19-JUL-1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Hoffmann-La Roche Inc.
33 REGISTRATION NUMBER: 32142
34 REFERENCE/DOCKET NUMBER: CD 9174
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (201) 235-4205
37 TELEFAX: (201) 235-3500
38 INFORMATION FOR SRQ ID NO: 5:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 572 amino acids
41 TYPE: amino acid
42 TOPOLOGY: 1 loop
43 MOLECULE TYPE: protein
44 FEATURE:
45 NAME/KEY: Region
46 LOCATION: 1..572
47 OTHER INFORMATION:
48 OTHER INFORMATION: 742 of human gp130.*
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50 US-08-419-652-5
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53 Best Local Similarity 100.0%: Prd. No.1,7e-14;
54 Matches 25: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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56 1 NPTLSSWATIRKFDCKAKRDTPTS 25
57 |||||||
58 DB 34 NPTLSSWATIRKFDCKAKRDTPTS 58

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QY      1  NPTLKSMAHREFADCKKRDPTTS  25
DB      34  NPTLKSMAHREFADCKKRDPTTS  58

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Best Local Similarity 100.0%  Pred. No. 1,7e-14;
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RESULT
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Sequence 4, Application US/08825558
Patent No. 5365724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLY A.
TITLE OF INVENTION: Cg 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, RESSLER, GOLDSTEIN & FOX
FIRM: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825 558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ASHOUN, ROBERT J.
FIRM: 3600 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-4

Query Match
US-08-825-558-4
Sequence 2, Application US/0797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
FIRM: 32111 1ST AVE
CITY: SEATTLE
STATE: WA
COUNTRY: USA
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0606
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match
US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
FIRM: 32111 1ST AVE
CITY: SEATTLE
STATE: WA
COUNTRY: USA
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

```

Query Match 100.0%: Score 139: DB 1: Length 708;
 Best Local Similarity 100.0%: Pred. No. 2, 1e-14;
 Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
 Oy 1 NPTLKSEWATKRFADCKARADPTPS 25
 ||||||||||||||||||||
 DB 157 NPTLKSEWATKRFADCKARADPTPS 181

RESULT 7
 US-09-058-263-2
 : Sequence 2, Application US/09058263
 : Patent No. 5891997
 : GENERAL INFORMATION:
 : APPLICANT: Mosley, Bruce
 : ATTORNEY/AGENT: David J. Receptor for Oncostatin M
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : PUBLICATION NO.: 5891010
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: Apple Macintosh
 : SOFTWARE: Microsoft Word, Version 5.1a
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/058,263
 : FILING DATE: 12-SEP-1994
 : PRIORITY/DATE: 26-MAY-1994
 : ATTORNEY/AGENT INFORMATION:
 : REGISTRATION NUMBER: 32,172
 : REFERENCE/DOCKET NUMBER: 2614-A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (206) 587-0430
 : TELEFAX: (206) 233-0644
 : TELEX: 756822
 : INFORMATION FOR SEQ. ID NO. 2:
 : SEQ. CHARACTERISTICS:
 : LENGTH: 708 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-09-058-263-2

Query Match 100.0%: Score 139: DB 2: Length 708;
 Best Local Similarity 100.0%: Pred. No. 2, 1e-14;
 Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
 Oy 1 NPTLKSEWATKRFADCKARADPTPS 25
 ||||||||||||||||||||
 DB 157 NPTLKSEWATKRFADCKARADPTPS 181

RESULT 8
 US-09-059-099-2
 : Sequence 2, Application US/09059099
 : Patent No. 5925740
 : GENERAL INFORMATION:
 : APPLICANT: Mosley, Bruce
 : ATTORNEY/AGENT: David J. Receptor for Oncostatin M
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : PUBLICATION NO.: 5925740
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: Apple Macintosh
 : SOFTWARE: Microsoft Word, Version 5.1a
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/059,099
 : FILING DATE: 12-SEP-1994

TITLE OF INVENTION: Receptor for Oncostatin M
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : PUBLICATION NO.: 5925740
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: Apple Macintosh
 : SOFTWARE: Microsoft Word, Version 5.1a
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/059,099
 : FILING DATE: 12-SEP-1994
 : PRIORITY/DATE: 26-MAY-1994
 : ATTORNEY/AGENT INFORMATION:
 : REGISTRATION NUMBER: 32,172
 : REFERENCE/DOCKET NUMBER: 2614-A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (206) 587-0430
 : TELEFAX: (206) 233-0644
 : TELEX: 756822
 : INFORMATION FOR SEQ. ID NO. 2:
 : SEQ. CHARACTERISTICS:
 : LENGTH: 708 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-09-059-099-2

Query Match 100.0%: Score 139: DB 2: Length 708;
 Best Local Similarity 100.0%: Pred. No. 2, 1e-14;
 Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
 Oy 1 NPTLKSEWATKRFADCKARADPTPS 25
 ||||||||||||||||||||
 DB 157 NPTLKSEWATKRFADCKARADPTPS 181

RESULT 9
 US-09-058-264-2
 : Sequence 2, Application US/09058264
 : Patent No. 6010886
 : GENERAL INFORMATION:
 : APPLICANT: Mosley, Bruce
 : ATTORNEY/AGENT: David J. Receptor for Oncostatin M
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : PUBLICATION NO.: 6010810
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: Apple Macintosh
 : SOFTWARE: Microsoft Word, Version 5.1a
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/058,264
 : FILING DATE: 12-SEP-1994


```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
PCT NUMBER: US/95/06530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 357-0430
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-058-264-2
NO DOCKET TYPE: protein

Query Match
Best Local Similarity 100.0%; Score 139; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLSSEWATHRFADCKAKRDPTFS 25
|||||
DB 157 NFKLSSEWATHRFADCKAKRDPTFS 181

RESULT 10
PCT-US95-06530-2
Sequence 2, Application PC/70S9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immune Corporation
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
SOFTWARE: PatentIn Release #1, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 12-SEP-1994
PCT NUMBER: US/95/06530
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 357-0430
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid

```

```

TOPOLGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match
Best Local Similarity 100.0%; Score 139; DB 5; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLSSEWATHRFADCKAKRDPTFS 25
|||||
DB 157 NFKLSSEWATHRFADCKAKRDPTFS 181

RESULT 11
US-08-825-558-6
Sequence 6, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
ADDRESSEE: SHARKEY, ANDREW K.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-6

Query Match
Best Local Similarity 100.0%; Score 139; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 2,8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLSSEWATHRFADCKAKRDPTFS 25
|||||
DB 157 NFKLSSEWATHRFADCKAKRDPTFS 181

RESULT 12
US-08-217-927-8
Sequence 7, Application US/08217327
Patent No. 5474925
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Immobilized proteins in cotton fiber

```

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESS: Quarles and Brady
 CITY: Madison
 STATE: WI
 COUNTRY: USA
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/217,327
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/812,233
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-221-5000
 TELEFAX: 608-221-5116
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 592 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-217-327-8

Query Match 33.1%; Score 46; DB 1; Length 592;
 Best Local Similarity 42.9%; Pred. No. 16;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 2 FLTKSEKATKFRACKAKKPT 22
 Db 41 YTIQSEKSTGTANTITLAKDT 61

RESULT 13
 US-08-910-313-2
 Sequence 2, Application US/08910313
 GENERAL INFORMATION:
 APPLICANT: Black, Michael Terence
 TITLE OF INVENTION: No. 617183861 RatB
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Dechert, Price & Rhoads
 STREET: 4000 Bell Atlantic Tower, 1717 Arch St
 CITY: Philadelphia
 STATE: PA
 COUNTRY: US
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/910,313
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Dickinson, Todd O
 REGISTRATION NUMBER: 28,0410072
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-994-2252
 TELEFAX: 215-994-2222
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-910-313-2

Query Match 30.6%; Score 42.5; DB 4; Length 488;
 Best Local Similarity 43.5%; Pred. No. 16;
 Matches 10; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
 Oy 1 NPTLKSPATKFRPD-CRKKRDT 22
 Db 347 NYRALSMTYVERGKCRKRGKT 369

RESULT 14
 US-08-665-405-28
 Sequence 28, Application US/08665405
 Patent No. 5874220
 GENERAL INFORMATION:
 APPLICANT: FACH, Patrick; GULLIQU
 APPLICANT: Jean-Pierre; POPOFF, Michael
 TITLE OF INVENTION: AMELIORATION OF GENES CODING FOR THE
 TITLE OF INVENTION: ENTEROTOXIN AND THE DELETION OF CLOSTRIDIUM
 TITLE OF INVENTION: PERFRINGENS AND THEIR APPLICATION TO THE
 TITLE OF INVENTION: DETECTION AND NUMERATION OF THESE BACTERIAE
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESS: BERMAN & MISERLIAN
 STREET: 500 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/666,405
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: SCT/EP94/04292
 FILING DATE: 22-DEC-1994
 APPLICATION DATA:
 FILING DATE: 22-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: MISERLIAN, CHARLES A
 REGISTRATION NUMBER: 9,1683
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8002
 TELEFAX: (212) 661-8000
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:36 ; Search time 170.68 seconds
(without alignments)
6.510 million cell updates/sec

Title:	US-09-202-104A-9
Perfect score:	81
Sequence:	1 WVEAENALGKVTSDH 15

Scoring table: BLOSUM62

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Maximum DB seq length: 2000000000

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post-processing: Minimum Match 0%
                  Maximum Match 100%

```

Listing first 45 summaries

Database :

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	81	100.0	15	19	AAW52209	Interleukin-6 ant
2	81	100.0	24	22	AAAB8836	Human Interleukin-6
3	81	100.0	329	18	AAW17859	Rheumatoid arthrit
4	81	100.0	332	21	AAW21888	Human gp130-delta
5	81	100.0	332	21	AAW21888	Human gp130-delta
6	81	100.0	658	17	AAAR34764	Human gp130 N-term
7	81	100.0	708	14	AAAR34764	Human gp130 N-term
8	81	100.0	708	17	AAAR59311	Human gp130 N-term
9	81	100.0	727	21	AAW52192	Human gp130-Kappa
10	81	100.0	738	21	AAW52192	Human gp130-Kappa
11	81	100.0	859	20	AAW92796	Human gp130-Fc-His

[illegible][illegible]

```

SO Sequence 332 AA:
Query Match 100.0%; Score 81; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 2,3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
    |||
Db 197 wveena1gkvtscd 211

RESULT 6
AAR94576
ID AAR94576 standard; Protein: 658 AA.
AC AAR94576;
NC 20-JUN-1996 (first entry)
DE Human gp130 splice variant.
XX
XX gp130: transmembrane domain; growth factor antagonist;
XX embryo preimplantation; in vitro fertilisation.
XX Homo sapiens.
XX MO9609382-A1.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95MO-G802243.
XX
XX 21-SEP-1994; 94GB-0019021.
XX
XX (ISTF ) ARS APPLIED RES SYST HOLDING NV.
XX
XX Dellow KA, Sharkey A, Smith SK;
XX
XX WPI: 1996-18844/19.
XX
XX N-PSDB: AA014602.
XX
XX New splice variant of gp130 lacking the trans-membrane domain -
XX useful as an antagonist for growth factors esp. for ensuring correct
XX development of pre-implantation embryos
XX
XX Example 2: Fig 1: 33pp; English.
XX
XX A novel, soluble splice variant (AAR94576) of human gp130 corresponds
XX to amino acids 1-613 of native gp130 (AAR95368) but has a novel
XX C-terminal sequence (AAR94575) from amino acid 614 onwards.
XX The splice variant lacks a transmembrane region. It was initially
XX detected during the morula to blastocyst transition of human
XX embryos. The splice variant antagonises the action of human
XX factors, e.g. interleukin-6, leukaemia inhibitory factor.
XX The soluble variant can be used to ensure correct
XX development of preimplantation embryos, patulo. for in vitro
XX fertilisation.
XX
XX Sequence 658 AA:

Query Match 100.0%; Score 81; DB 17; Length 658;
Best Local Similarity 100.0%; Pred. No. 2,3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
    |||
Db 197 wveena1gkvtscd 211

RESULT 7
AAR37804
ID AAR37804 standard; Protein: 708 AA.
AC AAR37804;
NC 01-OCT-1993 (first entry)
DE Human gp130 N-terminal fragment.
XX
XX Oncostatin M; leukaemia inhibitory factor; receptor; PCR; fusion;
XX LIF-R; gp130; linker.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX /label= sig-peptide
XX Protein 23..708
XX /label= mal-protein
XX Domain 23..319
XX /label= extracellular_domain
XX Region 620
XX /label= transmembrane_region
XX /note= "beginning with amino acid 620"
XX Domain 643..708
XX /label= cytoplasmic_domain
XX /note= "partial cytoplasmic domain"
XX
XX Misc-difference 8
XX /note= "differs from the equv. portion of the Hb1
XX et al. Cell 63:1149 (1990) protein in that
XX the eighth amino acid of the signal sequence
XX is Leu rather than Val."
XX
XX MO9310151-A.
XX
XX 27-MAY-1993.
XX
XX 20-NOV-1992; 92MO-0510272.
XX
XX 22-NOV-1991; 91US-0797556.
XX
XX (IMM V ) IMMUNEX CORP.
XX
XX gearing DP;
XX
XX WPI: 1993-182493/22.
XX
XX N-PSDB: AAQ42588.
XX
XX Receptor protein comprising gp130 covalently linked to LIF
XX protein and fused to a polypeptide useful for treating
XX Kaposi's sarcoma, atherosclerosis, obesity etc.
XX
XX Disclosure: Page 48-53; 79pp; English.
XX
XX A new receptor (R), able to bind oncostatin M and leukaemia
XX inhibitory factor (LIF), comprising a gp130 polypeptide (AAQ42588)
XX fused to a polypeptide (AAQ42589) for example
XX suitable region of an inhibitory polypeptide amino acids 22-528, 22-320,
XX 120-320 etc., or lack all or part of the transmembrane region
XX and/or cytoplasmic domain.
XX Pref. both components of (R) are soluble proteins and are connected
XX by a polypeptide linker of 20-100 amino acids consisting of Gly, Asn,
XX Ser, Thr or Ala.
XX
XX Sequence 708 AA:

Query Match 100.0%; Score 81; DB 14; Length 708;
Best Local Similarity 100.0%; Pred. No. 5,5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
    |||

```


DB 197 wveanalgyvtsdh 211

RESULT 8

AA85911 ID AA85911 standard; Protein; 708 AA.

AA85911:

03-JUL-1996 (first entry)

gp130 N-terminal fragment.

Human: gp130: inhibitor; oncostatin M; cytokine; antibody Fc region; oncostatin M receptor-beta chain; antibody; tumour; growth factor; therapy.

Homo sapiens.

Key

Peptide 1 location/Qualifiers

23..708 /note="signal peptide"

Modified-site 21..23 /note="N-terminal fragment of mature gp130"

Modified-site 61..63 /note="glycosylation site"

Modified-site 109..111 /note="glycosylation site"

Modified-site 135..137 /note="glycosylation site"

Cleavage-site 153..154 /note="glycosylation site"

Modified-site 205..207 /note="glycosylation site"

Modified-site 229..235 /note="glycosylation site"

Modified-site 357..359 /note="glycosylation site"

Modified-site 361..363 /note="glycosylation site"

Modified-site 368..370 /note="glycosylation site"

Modified-site 542..544 /note="glycosylation site"

Cleavage-site 621..622 /note="glycosylation site"

W09533059-A2.

07-DEC-1995.

22-MAY-1995; 95MO-US06530.

12-SEP-1994; 94US-0308881.

26-MAY-1994; 94US-0249553..

(IMMAY) IMMUNEX CORP.

Cosman DJ; Mosley B;

WPI: 1996-030570/03.

N-PSDB: A0074081.

Heater: dimeric receptor proteins comprising OSK-R beta and gp 130 - heterodimeric receptor proteins comprising OSK-R beta and gp 130 - mediated by oncostatin M

Claim 1: Page 35-38; 60pp: English.

This sequence represents an N-terminal fragment of gp130 obtained from human placenta. gp130 binds to oncostatin M, which is a secreted single

CC chain polypeptide cytokine. Oncostatin M regulates the growth of

CC certain tumour derived and normal cell lines. This receptor protein, and

CC the oncostatin M receptor-beta chain (see AA85912) sequence can be

CC used to identify and purify the receptor. The receptor is capable of

CC binding to oncostatin M. The receptors can also comprise fusion

CC polypeptides, where an antibody Fc region is joined to the C-terminus of

CC each of the soluble proteins. In this case, the two fusion polypeptides

CC are joined by disulphide bonds between the two antibody Fc regions. The

CC heterodimeric receptors can be used to inhibit biological activities

CC mediated by oncostatin M. The advantage with using the heterodimeric

CC receptors is that they bind to oncostatin M at greater levels than gp130

CC does alone.

SO Sequence 708 AA:

Query Match 100.0%; Score 81; DB 17; Length 708;

Best Local Similarity 100.0%; Pred. No. 5,5e-06;

Matches 15; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYAEANALGYVTSDH 15

|||||

DB 197 wveanalgyvtsdh 211

RESULT 9

AA92192 ID AA92192 standard; protein; 727 AA.

AA92192:

01-AUG-2000 (first entry)

Human gp130-kappa domain fusion protein.

gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;

cytokine; immunomodulator; osteopathic.

Synthetic.

Homo sapiens.

Key

Protein 1..619 location/Qualifiers

Peptide 1..619 /label="gp130"

Protein 622..727 /note="Ser-Gly bridge"

Protein /label="IgG1_kappa_domain"

W0200018932-A2.

06-APR-2000.

22-SEP-1999; 99MO-US22045.

25-SEP-1998; 98US-0101858.

19-MAY-1999; 99US-0313942.

(REGG-) REGENERON PHARM INC.

Stahl N; Yancopoulos GD;

WPI: 2000-293165/25.

Isolated nucleic acid molecule for treating cytokine-related diseases

or disorders encodes a fusion polypeptide capable of binding a cytokine

to form a nonfunctional complex

Example 4: Page -; 152pp: English.

The invention concerns production of antagonists to any cytokine that

utilizes an alpha specificity determining component, which when combined

with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specifically determining component first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (alpha-beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (cellary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that IL-6
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine membrane-bound forms of their receptor, thus the nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC NB. This sequence was constructed from the gp130 and kappa domain
 CC sequences given in Figures 9 and 13 of the specification.
 CC
 CC Sequence 727 AA:
 50
 Query Match 100.0%; Score 81; DB 21; Length 727;
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WVEARNALQVTSQH 15
 197 WVEARNALQVTSQH 211
 Db
 RESULT 10
 AA92194
 ID AAT92194 standard; protein: 738 AA.
 AC AAT92194;
 XX
 DT 01-AUG-2000 (first entry)
 DE Human gp130-J-kappa fusion protein.
 DD
 XX gp130-J-kappa; cytokine; antagonist; CNTF; receptor; fusion protein;
 XX cytosolic; immunomodulator; osteopontic.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FI Key Location/Qualifiers
 FI Protein 1..619
 FI Peptide 6200018932-A2
 FI Peptide /note="Ser-Gly bridge"
 FI Peptide 622..632
 FI Peptide /note="J-peptide"
 FI Peptide 633..738
 FI Domain /label="Kappa-domain"
 XX
 XX MO200018932-A2.
 XX
 XX 06-APR-2000.
 XX
 XX 22-SEP-1999; 99MO-US22045.
 XX
 XX 25-SEP-1998; 98DS-0101856.
 XX PR 19-MAY-1999; 98DS-0313942.
 XX
 XX (RBCF-) REGENERON PHARMA INC.

XX Stahl N, Yancopoulos GD;
 XX WPL: 2000-293165/25.
 DR
 XX Isolated nucleic acid molecule for treating cytokine-related diseases
 PF or disorders encodes a fusion polypeptide capable of binding a cytokine
 PF to form a nonfunctional complex
 XX
 XX Example 4; Page --: 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component
 CC to form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing component of the receptor, the
 CC (alpha-beta-1) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (alpha-beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (cellary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that IL-6
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine membrane-bound forms of their receptor, thus the nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC
 CC Sequence 738 AA:
 50
 Query Match 100.0%; Score 81; DB 21; Length 738;
 Best Local Similarity 100.0%; Pred. No. 5.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WVEARNALQVTSQH 15
 197 WVEARNALQVTSQH 211
 Db
 RESULT 11
 AAM70796
 ID AAM70796 standard; protein: 859 AA.
 AC AAM70796;
 XX
 XX 03-FEB-1999 (first entry)
 DE Human gp130-Fc-His6 amino acid sequence.
 DD
 XX gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 FI Key Location/Qualifiers
 FI Protein 1..619
 FI Peptide /note="human gp130"
 FI Misc-difference 2
 FI /label="L2Y"
 FI /note="amino acid changed to accommodate a Kozak
 FI sequence"

```

FT Peptide 1..22 /note="signal peptide"
FT Misc-difference 620..621 /label= gp130
FT Protein /note="Ser-Gly bridge"
FT Disulfide-bond 632..635 /note="from the FC domain of human IgG1"
FT Peptide 854..859 /note="hexahistidine tag"
XX US5844099-A.
XX 01-DEC-1998.
XX 27-NOV-1995; 95US-0563105.
XX 27-NOV-1995; 95US-0563105.
PR 20-OCT-1993; 93US-0140222.
XX (REG3-) REGENERON PHARM INC.
XX Economidis A, Stahl N, Yancopoulos GD;
XX WPI; 1999-044669/04.
XX Cytokine antagonists - comprising extracellular domains of
XX specificity-determining and signal-transducing components of
XX cytokine receptor
XX Example 3; Fig 4; 46pp; English.
XX The present sequence represents the amino acid sequence of human
XX gp130-FC-His6. The protein is used in the course of the invention. The
XX extracellular domain of the specificity-determining component of
XX the cytokine receptor and the specificity-determining component of
XX signal-transducing component of the cytokine receptor are fused to
XX form a non-functional intermediate which then binds to a second beta
XX signal-transducing component causing beta-receptor dimerization. The
XX signal-transducing component of the first beta signal
XX transducing component of the cytokine receptor (beta-1) are combined to
XX form heterodimers (sr-alpha:beta-1) that act as antagonists to the
XX cytokine by binding the cytokine to form a non-functional complex. The
XX receptor components are shared by cytokines such as the CNTF (ciliary
XX neurotrophic factor) family of cytokines. The invention provides the
XX presence of a ligand, a non-functional intermediate complex,
XX consisting of the ligand, its alpha receptor and its beta-1 receptor
XX component, can be formed, it will effectively block the action of the
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX of the extracellular domains of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130
XX consisting of the extracellular domain of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130
XX native membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia.
XX Sequence 859 AA:
XX
XX Query Match 100.0%; Score 81; DB 20; Length 859.
XX Best Local Similarity 100.0%; Pred. No. 6,8e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 WYENALGKWTSDH 15
XX Db 197 WVENALGKWTSDH 211

```

```

FH Key Location/Qualifiers
FH Protein 1..619
FH Peptide /label= gp130
FH Peptide 1..22 /label= signal-peptide
FH Peptide 620..621 /note="Ser-Gly bridge"
FH Disulfide-bond 632 /note="forms inter-chain disulfide bridge that
FH /note="link two FC domains"
FH Disulfide-bond 635 /note="forms inter-chain disulfide bridge that
FH /note="link two FC domains"
FH Protein /label= gp130
FH Peptide /label= gp130-FC-domain
FH Peptide 854..859 /label= histidine-tag
XX WO200018932-A2.
XX 06-APR-2000.
XX 22-SEP-1999; 99WO-US22045.
XX 25-SEP-1998; 98US-0101858.
XX 19-MAY-1999; 99US-0313942.
XX (REG3-) REGENERON PHARM INC.
XX Stahl N, Yancopoulos GD;
XX WPI; 2000-293165/25.
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX Example 3; Fig 4; 15pp; English.
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal-transducing component causing beta-receptor dimerization. The
XX signal-transducing component of the first beta signal
XX transducing component of the cytokine receptor (beta-1) are combined to
XX form heterodimers (sr-alpha:beta-1) that act as antagonists to the
XX cytokine by binding the cytokine to form a non-functional complex. The
XX receptor components are shared by cytokines such as the CNTF (ciliary
XX neurotrophic factor) family of cytokines. The invention provides the
XX presence of a ligand, a non-functional intermediate complex,
XX consisting of the ligand, its alpha receptor and its beta-1 receptor
XX component, can be formed, it will effectively block the action of the
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX of the extracellular domains of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130
XX consisting of the extracellular domain of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130
XX native membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia.
XX Sequence 859 AA:
XX
XX Query Match 100.0%; Score 81; DB 21; Length 859.
XX Best Local Similarity 100.0%; Pred. No. 6,8e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 WYENALGKWTSDH 15

```

Db 197 wveena1gkvtstdh 211

RESULT 13

AAAR10545 standard; Protein: 918 AA.

AAAR10545:

12-APR-1991 (first entry)

Recombinant human gp130 protein.

Recombinant human gp130; interleukin-6; interleukin-6 receptor; immunity; hematopoiesis; inflammation; therapy.

Homo sapiens.

EP411946-A.

06-FEB-1991.

02-AUG-1990: 90BP-0308530.

31-MAY-1990: 90BP-0140059.

03-AUG-1989: 89BP-0200230.

(KISH)/ KISHIMOTO T.

Kishimoto T;

WPI: 1991-030820/06.

N-PSDB: AAQ20402.

Recombinant human gp130 protein - acts in the transmission of interleukin-6 signal for defence mechanisms

Disclosure: fig 7: 32pp; English.

This gp130 protein is produced using standard recombinant DNA technology (gp130-1990). It is a fusion of the gp130 protein with a standard human protein. It participates in the transmission of the interleukin (IL)-6 signal, and therefore the proliferation and differentiation of an organism. It is important in an animals defence mechanisms, e.g. immunity, hematopoiesis and inflammation.

Sequence 918 AA:

Query Match 100.0%; Score 81; DB 12; Length 918;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEENALGKVTSDH 15

Db 197 wveena1gkvtstdh 211

RESULT 14

AAAR6233 standard; Protein: 918 AA.

AAAR6233:

15-SEP-1994 (first entry)

Human soluble glycoprotein (gp) 130.

Glycoprotein: soluble; gp: gp130; antibody production; assay.

Immunological assay; detection; immunogen; transmembrane domain.

Homo sapiens.

XX JP6022786-A.

XX 01-FEB-1994.

XX 02-AUG-1991: 91BP-0217924.

XX 02-AUG-1991: 91BP-0217924.

XX (KISH)/ KISHIMOTO C.

XX (TOYO) TOSOH CORP.

XX WPI: 1994-071006/09.

XX N-PSDB: AAQ56931.

XX Preparation of recombinant soluble human gp 130 deriv - for use in the production of anti-gp 130 antibody for immunochemical assay

XX Claim 1: Figure 7: 13pp; Japanese.

XX The soluble glycoprotein (gp) 130 can be used as an immunogen for the preparation of anti-gp130 antibody. A standard substance for immunochemical assay is prepared by inserting a gp130 cDNA was prepared or transmembrane domain prior to the extracellular domain or transmembrane domain of the gp130 coding sequence or simply by eliminating the transmembrane domain.

XX Sequence 918 AA:

Query Match 100.0%; Score 81; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEENALGKVTSDH 15

Db 197 wveena1gkvtstdh 211

RESULT 15

AAAR75368 standard; Protein: 918 AA.

AAAR75368:

20-JUN-1996 (first entry)

Human gp130 protein.

Gp130; transmembrane domain; growth factor antagonist;

embryo pre-implantation; in vitro fertilisation.

Homo sapiens.

Key Location/Qualifiers
620..641
Region /label= Transmembrane-region

XX WO5609382-A1.

XX 28-MAR-1996.

XX 21-SEP-1995: 95MO-GB02243.

XX 21-SEP-1994: 94GB-0019021.

XX (ISTF) ARS APPLIED RES SYST HOLDING NV.

XX Dellow KA, Sharkey A, Smith SF;

XX WPI: 1996-18444/19.

XX N-PSDB: AART4603.

XX New splice variant of gp130 lacking the trans-membrane domain
 PT useful as an antagonist for growth factors esp. for ensuring correct
 PT development of pre-implantation embryos
 XX
 PS Disclosure; Fig 2; 33pp; English.
 XX
 CC A DNA sequence (AAT14603) codes for native human gp130 (AAR75368).
 CC A novel splice variant (see AAT14602) that lacks the transmembrane
 CC region was identified in the morula to blastocyst transition stage
 CC of the human embryo. The splice variant antagonises the action
 CC of certain growth factors and can be used to ensure correct
 CC development of preimplantation embryos.
 XX
 SO Sequence 918 AA;

Query Match 100.0%; Score 81; DB 17; Length 918;
 Best Local Similarity 100.0%; Pred. No. 7,4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WVEAENALGKVTSDH 15
 |||||
 DB 197 wveaenalgkvtstdh 211

Search completed: December 19, 2001, 16:19:36
 Job time: 361 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:40 ; Search time 88.82 seconds
(without alignments)
12,864 Million cell updates/sec

File: us-09-202-104a-9

Sequence: 1 WVEAENALGKVTSDH 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first: 45 summaries

Database :

1: PIR:68:*
2: PIR:2:*
3: PIR:3:*
4: PIR:4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of this result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	918	2	membrane glycoprot
2	65	80.2	917	2	glycoprotein 130 -
3	60	74.1	918	2	interleukin-6 sign
4	46	56.8	771	2	granulocyte colony
5	46	56.8	783	2	granulocyte colony
6	46	56.8	863	2	granulocyte colony
7	42	51.9	170	2	hypothetical prote
8	42	51.9	170	2	probable integrase
9	42	51.9	643	2	RNA polymerase s1g
10	42	51.9	642	2	granulocyte colony
11	42	51.9	837	2	hypothetical prote
12	41	50.6	148	1	k1ab protein - pla
13	41	50.6	237	2	hypothetical prote
14	41	50.6	264	2	hypothetical prote
15	41	50.6	386	2	hypothetical prote
16	41	50.6	1032	2	hypothetical prote
17	41	50.6	1032	2	hypothetical prote
18	40	49.4	1462	1	DMN-directed DNM p
19	40	49.4	1462	1	prolyl endopeptida
20	39.5	48.8	686	2	transcription elon
21	39	48.1	161	2	hypothetical prote
22	39	48.1	269	2	cardiomyo1-phosphat
23	39	48.1	377	2	multidrug resistanc
24	39	48.1	422	2	tubulin gamma chain
25	39	48.1	468	2	tubulin gamma chain
26	39	48.1	507	2	hypothetical prote
27	39	48.1	507	2	myo-inositol cata
28	39	48.1	637	2	
29	39	48.1	637	2	

30	39	48.1	952	2	hypothetical prote
31	38.5	47.5	240	2	transposase - Sp1r
32	38	46.9	1113	2	conserved hypothet
33	38	46.9	1113	2	hypothetical prote
34	38	46.9	1113	2	hypothetical prote
35	38	46.9	211	2	hypothetical prote
36	38	46.9	220	2	hypothetical prote
37	38	46.9	264	2	hypothetical prote
38	38	46.9	426	2	protoporphyrin IX
39	38	46.9	426	2	probable trehalase
40	38	46.9	533	2	hypothetical prote
41	38	46.9	630	2	prolactin receptor
42	38	46.9	704	2	DMN-directed DNM p
43	38	46.9	909	2	nitrate reductase
44	38	46.9	1109	2	probable disease r
45	38	46.9	1109	2	

ALIGNMENTS

RESULT 1
A:36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
G:Accession: A36337
E:Accession: A36337 M.: Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Ref:63 1149-1157,1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: RNA
A:Residues: 1-918 <R18>
A:Cross-references: GB:M57230; MTD:q186353; PTDN:AA59155.1; PID:q186354
A:Gene: CDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 100.0% Score 81: DB 2: Length 918;
Best Local Similarity 100.0%; Pred. No. 3, Re-06;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WVEAENALGKVTSDH 15
Db 197 WVEAENALGKVTSDH 211
|||||
Db 197 WVEAENALGKVTSDH 211

RESULT 2
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
G:Accession: U45839; 14837 Ribi, M.; Taga, T.; Kishimoto, T.
E:Accession: U45839; 14837 Ribi, M.; Taga, T.; Kishimoto, T.
J:Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130.
A:Reference number: 148370; MUID:92291532
A:Accession: 145699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <R2>
A:Cross-references: GB:M83336; MTD:q193591; PTDN:AA37723.1; PID:q193592
A:Accession: 148370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <R2>

A/Cross-references: GB:S71484; NID:g240883; PIDN:AB20560.1; PID:g240884
 A:Experimental source: granulocyte
 A:Note: Sequence extracted from NCB1 backbone (NCBI:71488, NCBI:71485)
 A:Accession: C58822
 A:Species: *Escherichia coli*
 A:Molecule type: DNA
 Arch. Blochm. Biophys. 324, 344-356, 1995
 A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
 A:Reference number: S68331; MUID:56132662
 A:Accession: S68332
 A:Molecule type: protein
 A:Residues: 234-269 <MAN>
 C:Gene: *CSF3R*
 A:Cross-references: GB:1256430; OMIM:138971
 A:Map position: 1p35-p34.3
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-34/Domains: signal sequence *status predicted <S>
 F:25-863/Product: granulocyte colony-stimulating factor receptor, long form *status pred
 F:25-680/708-863/Product: granulocyte colony-stimulating factor receptor, short form *st
 F:25-627/Domains: extracellular *status predicted <S>
 F:25-627/Domains: intracellular *status predicted <S>
 F:654-863/Domains: intracellular *status predicted <S>
 F:93,128,134,389,474,579,610/Binding site: carbohydrate (asn) (covalent) *status predict

Query Match 56.8%; Score 46; DB 2; Length 863;
 Best Local Similarity 68.9%; Pred. No. 6.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVENALMG 9
 11:|||||

DB 202 WVOANALG 210

RESULT 7
 F83807
 A:Protein: hypothetical protein 2950 [Imported] - *Escherichia coli* (strain O157:H7)
 A:Accession: F83807
 A:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: F83807
 R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: F83807
 A:Accession: F83807
 A:Residues: 1-170 <STO>
 A:Molecule type: DNA
 A:Status: preliminary
 A:Cross-references: GB:AE005174; NID:g12516002; PIDN:AG56922.1; GSPPB:GN00145; UWGP:Z25
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Gene: *EHEC290*
 C:Superfamily: Pseudomonas aeruginosa hypothetical protein FTR2

Query Match 51.9%; Score 42; DB 2; Length 170;
 Best Local Similarity 61.9%; Pred. No. 5.3;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVENALMGKVTIS 13
 11:|||||

DB 13 FVDCNEVKGKVS 25

RESULT 8
 C58822
 A:Gene: integrase for prophage CP-9330 Int0 [Imported] - *Escherichia coli* (strain O157:
 C:Accession: C58822
 A:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: AB5480; MUID:21074935; PMID:11206551
 A:Accession: C58822
 A:Species: *Escherichia coli*
 A:Molecule type: DNA
 A:Residues: 1-340 <STO>
 A:Cross-references: GB:AE005174; NID:g12516149; PIDN:AG57039.1; GSPPB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Gene: *Int0*

Query Match 51.9%; Score 42; DB 2; Length 340;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WVENALMGKVTIS 12
 264 WVENALMGKVTIS 275

RESULT 9
 AB1798
 RNA polymerase sigma factor NMA1737 [Imported] - *Neisseria meningitidis* (strain 22491
 C:Species: *Neisseria meningitidis*
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: AB1798
 R:Holroyd, S.; Kemp, M.; Times, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491
 A:Reference number: AB1775; MUID:20222556
 A:Accession: AB1798
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-642 <MAN>
 A:Cross-references: GB:AL162757; GB:AL159559; NID:g7380371; PIDN:CB84956.1; PID:g738
 A:Experimental source: serogroup A, strain 22491
 C:Gene: *sigma*
 C:Superfamily: transcription initiation factor sigma 70; transcription initiation fac

Query Match 51.9%; Score 42; DB 2; Length 642;
 Best Local Similarity 57.1%; Pred. No. 24;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 WVENALMGKVTIS 14
 339 WVEEALMGKVTIS 352

RESULT 10
 F81072
 RNA polymerase sigma factor RPOD NMB1538 [Imported] - *Neisseria meningitidis* (strain
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: F81072
 R:Perleberg, H.; Sundberg, N.J.; Beideldberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen
 Science 287, 1809-1815, 2000
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: AB1000; MUID:2015755
 A:Accession: F81072
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-642 <STO>
 A:Cross-references: GB:AE002503; GB:AE002096; NID:g7226775; PIDN:AAFA1893.1; PID:g722
 A:Experimental source: serogroup B, strain MC58
 C:Gene: *sigma*
 C:Superfamily: transcription initiation factor sigma 70; transcription initiation fac

Query Match 50.6%; Score 41; DB 2; Length 536;
Best Local Similarity 42.9%; Pred. No. 29;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 WVEANALKVTSD 14
||:|:::||||
Db 97 WVOEYNSVNEITSD 110

Search completed: December 19, 2001, 16:22:41
Job time: 401 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 19, 2001, 16:26:18 ; Search time 48.45 seconds
(without alignments)

11.351 Million cell updates/sec

Title: US-09-202-104a-9

Sequence: I WYEFANNAKXTSDH 15

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	918	1	IL6B_HUMAN
2	65	80.2	917	1	IL6B_MOUSE
3	40	54.1	916	1	IL6B_RAT
4	38	53.9	917	1	IL6B_MOUSE
5	42	53.9	837	1	IL6B_MOUSE
6	41	50.6	461	1	IL6B_MOUSE
7	40	50.6	580	1	IL6B_MOUSE
8	40	49.4	1462	1	DPO4_HUMAN
9	39	48.1	468	1	TG6_CHLRE
10	38	46.9	211	1	YOR3_SOYB
11	38	46.9	426	1	CHL1_TOBAC
12	38	46.9	680	1	YPR1_YEAST
13	38	46.9	680	1	YPR1_YEAST
14	38	46.9	704	1	DPO4_MOUSE
15	38	46.9	909	1	DPO4_MOUSE
16	37	45.7	92	1	NOPE_RHIV
17	37	45.7	186	1	YALD_TRYBIB
18	37	45.7	234	1	OPF5_METRO
19	37	45.7	234	1	OPF5_METRO
20	37	45.7	642	1	BPSD_METRO
21	37	45.7	825	1	BPSD_METRO
22	37	45.7	889	1	NIA3_MAZE
23	37	45.7	1053	1	CARP_STYPE
24	37	45.7	1192	1	IMG2_MOUSE
25	37	45.7	1301	1	SAC3_YEAST
26	37	45.7	1301	1	SAC3_YEAST
27	37	45.7	1301	1	SAC3_YEAST
28	37	45.7	1301	1	SAC3_YEAST
29	37	45.7	1301	1	SAC3_YEAST
30	36	44.4	68	1	HYVA_RHOCA
31	36	44.4	102	1	GCSH_CHICK
32	36	44.4	164	1	GCSH_CHICK
33	36	44.4	173	1	GCSH_CHICK

ALIGNMENTS

RESULT 1	ID	IL6B_HUMAN	STANDARD	PRF	918 AA.
34	36	44.4	299	1	Y13_MYCTU
35	36	44.4	384	1	MYR1_HABIN
36	36	44.4	384	1	POGE_METEX
37	36	44.4	687	1	CTCK_RABIT
38	36	44.4	755	1	NRG2_MOUSE
39	36	44.4	778	1	ACOR_YEAST
40	36	44.4	814	1	CAD2_HUMAN
41	36	44.4	850	1	NRG2_HUMAN
42	36	44.4	868	1	NRG2_MOUSE
43	36	44.4	879	1	MANB_CAPI
44	36	44.4	882	1	ALNS_PSEOL
45	36	44.4	882	1	ALNS_PSEOL

RESULT 1	ID	IL6B_HUMAN	STANDARD	PRF	918 AA.
34	36	44.4	299	1	Y13_MYCTU
35	36	44.4	384	1	MYR1_HABIN
36	36	44.4	384	1	POGE_METEX
37	36	44.4	687	1	CTCK_RABIT
38	36	44.4	755	1	NRG2_MOUSE
39	36	44.4	778	1	ACOR_YEAST
40	36	44.4	814	1	CAD2_HUMAN
41	36	44.4	850	1	NRG2_HUMAN
42	36	44.4	868	1	NRG2_MOUSE
43	36	44.4	879	1	MANB_CAPI
44	36	44.4	882	1	ALNS_PSEOL
45	36	44.4	882	1	ALNS_PSEOL

DR	InterPro:	IPR001996; CR1A.
DR	InterPro:	IPR001777; FN_III1.
DR	InterPro:	IPR003529; Hematopo_receptor_L_P2.
DR	SMART:	SM00060; FN1_3.
DR	PROSITE:	PS01353; HBMAPOPO_REC_L_FZ_1.
KW	Repeat:	
KW	Signal:	1; 22
FT	CHAIN	23 918
FT	DOMAIN	23 918
FT	INTERLEUDIN-6 RECEPTOR BETA CHAIN.	
FT	EXTRACELLULAR (POTENTIAL).	
FT	CYTOPLASMIC (POTENTIAL).	
FT	IG-LIKE C2-TYPE DOMAIN	619 518
FT	FIBRONECTIN TYPE-II 1.	124 221
FT	FIBRONECTIN TYPE-II 2.	222 333
FT	FIBRONECTIN TYPE-II 3.	424 422
FT	FIBRONECTIN TYPE-II 4.	432 516
FT	FIBRONECTIN TYPE-III 5.	517 612
FT	BY SIMILARITY.	728 74
FT	DISULFID	48 103
FT	BY SIMILARITY.	134 144
FT	DISULFID	172 181
FT	BY SIMILARITY.	457 465
FT	DISULFID	457 465
FT	N-LINKED (GLC.NG.)	43 43
FT	N-LINKED (GLC.NG.)	61 61
FT	N-LINKED (GLC.NG.)	81 81
FT	N-LINKED (GLC.NG.)	131 131
FT	N-LINKED (GLC.NG.)	157 157
FT	N-LINKED (GLC.NG.)	205 205
FT	N-LINKED (GLC.NG.)	226 226
FT	N-LINKED (GLC.NG.)	382 382
FT	N-LINKED (GLC.NG.)	389 389
FT	N-LINKED (GLC.NG.)	452 452
FT	N-LINKED (GLC.NG.)	552 552
SO	SOURCE	918 AA; 102450 NM; 9P1BBPDCRP087 CMO64;
Db	Query Match	Best Local Similarity 78.1%; Score 60; DB 1; Length 918; Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0.
Oy	1 WRENALACTVSD 14	
Db	196 WRENALACTVSSE 209	
RESULT	4	
ID	GCSR_HUMAN	STANDARD: PRT; 836 AA.
Dc	Q9J062.1995 (Rel. 31. Created)	
Dt	01-FEB-1995 (Rel. 31, last annotation update)	
Dt	20-AUG-2001 (Rel. 40, last annotation update)	
DE	GRAUOLCYTE COLONY STIMULATING FACTOR PRECURSOR (c-CSF-R)	
DE	(CD114 ANTIGEN)	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;	
OC	Mammalia; Primates; Primates; Catarrhini; Hominoidea; Homo.	
OX	NCBI_TaxId=9606;	
RN	[1]	
Rn	SEQUENCE FROM N.A.	
RX	TISSUE=Placenta;	
RX	MEDLINE=91079797; PubMed=2147944;	
RA	Larson A., Davis T., Curtis B.M., Lacey S.A., Lacey-Stumpe D., Larson L., Stenman E., March C.J., Smith C.S., Cosman D.,	
RA	Expression cloning identifies a novel member of hematopoietin receptor,	
RA	immunoglobulin, and fibronectin domains".	
RL	J. exp. Med. 172:1559-1570(1990).	
NN	[2]	

AC G9P6V6: 2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE THEONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA LIGASE)
 DN (THRS).
 DE THRS OR U0534.
 CS Ureaplasma parvum (Ureaplasma biocty 1).
 OS Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 NCBI TaxID=134821.
 RX MEDLINE=134821.
 RP SEQUENCE FROM N.A.
 RA STRAIN=SEROVA 3;
 RA MEDLINE=20500219; PubMed=11048724;
 RA Glass J. I., Lefkowitz E. J., Glass J. S., Helner C. R., Chan E. Y.,
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 urealyticum.".
 RL Nature 407:751-762(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + L-THREONINE + TRNA(THR) = AMP +
 PYROPHOSPHATE + L-THREONYL-TRNA(THR).
 CC -1- CORYCTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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DR EMBL: AE002152; AAC30947.1.
 DR InterPro: IPR002314; RNA-synchr.
 DR Pfam: PF00357; RNA-synchr.
 DR Pfam: PF00357; RNA-synchr.
 DR PROSITE: PS00179; AA-TRNA LIGASE II.1; FALSE NEG.
 DR PROSITE: PS00339; AA-TRNA LIGASE II.1; FALSE NEG.
 DR AMINOACYL-TRNA SYNTHETASE: Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Zinc: Complete proteome.
 FT DOMAIN 179 476
 FT METAL 272 272 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 323 323 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 423 423 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 453 453 ZINC (CATALYTIC) (BY SIMILARITY).
 FT SEQUENCE 580 AA; 67751 MW; 328C6F3A9D662E16 CRC64;

Query Match 50.6%; Score 41; DB 1; Length 580;
 Best Local Similarity 40.0%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Y7 1 WPEKNA.LCXYTSDH 15
 DB 376 WQSNV.LKMKLDH 390

RESULT 8
 DPOA.HUMAN STANDARD; PRT; 1462 AA.
 AC 01-MAR-1989 (Rel. 10, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DNA POLYMERASE ALPHA CATALYTIC SUBUNIT (EC 2.7.7.7).
 GN POLA.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OS Mammalia; Eumetazoa; Primates; Catarrhini; Hominoidea; Homo.
 NCBI TaxID=9606;

TX SEQUENCE FROM N.A.
 RX MEDLINE=48196090; PubMed=3359994;
 RA Wong S. W., Wahl A. F., Yuan P.-N., Aral N., Pearson B. E., Aral K.,
 RA Korn D., Hunkapiller M. W., Wang T. S. F.,
 RT "Human DNA polymerase alpha gene expression is cell proliferative
 dependent and its primary structure is similar to both prokaryotic
 RT and eukaryotic replicative DNA polymerases.".
 RN Mol. Cell Biol. 7:37-47(1986).
 RP SEQUENCE OF 1-8 FROM N.A.
 RA MEDLINE=91172197; PubMed=20058995;
 RA Pearson B. E., Nasheuer H. P., Wang T. S.,
 RT "Human DNA polymerase alpha gene: sequences controlling expression in
 RT cycling and serum-stimulated cells."
 CC -1- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMEASE IS A
 CC -1- REPLICATIVE POLYMERASE.
 CC -1- CATALYTIC ACTIVITY: N DEOXYRIBONUCLEOSIDE TRIPHOSPHATE =
 CC N PYROPHOSPHATE + DNA(N).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC ALPHA, BETA, GAMMA, DELTA, AND Epsilon WHICH ARE RESPONSIBLE FOR
 CC -1- MISCELLANEOUS: CONSERVED REGIONS II', IV, III AND I ARE THOUGHT TO
 CC BE INVOLVED IN SUBSTRATE RECOGNITION, BINDING OR PP(1) HYDROLYSIS.
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
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DR EMBL: X06745; CA629920.1.
 DR EMBL: X06745; CA629920.1.
 DR EMBL: X06745; CA629920.1.
 DR EMBL: X06745; CA629920.1.
 DR InterPro: IPR002064; DNA-pol.B.
 DR Pfam: PF00136; DNA-pol.B. 1.
 DR PRINTS: PR00106; DNAPOLB.
 DR SMART: SM00486; POLBc.1.
 DR PROSITE: PS00116; DNA-POLYMERASE-B.1.
 DR TRANSFERASE: DNA-directed DNA polymerase; DNA replication;
 KW DNA binding; 650 716
 FT DNA BIND 1245 1376
 FT SEQUENCE 1462 AA; 165860 MW; 25C2708A0DB38BE CRC64;

Query Match 49.4%; Score 40; DB 1; Length 1462;
 Best Local Similarity 61.5%; Pred. No. 47;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Y7 3 WPEKNA.LCXYTSDH 15
 DB 1400 DAECALEKLTJTH 1412

RESULT 9
 DPOA.HUMAN STANDARD; PRT; 468 AA.
 AC 03-SEP-82; 022417.
 DT 20-AUG-2001 (Rel. 40, Created)
 DE 20-AUG-2001 (Rel. 40, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TUBULIN GAMMA CHAIN (GAMMA TUBULIN).
 GN TUBG OR TUBG OR TBCA.
 OS Chlamydomonas reinhardtii.
 OS Chlamydomonas reinhardtii.
 OS Chlamydomonas reinhardtii.
 OS Chlamydomonadaceae; Chlamydomonadales; Volvocales;
 CC Chlamydomonadaceae; Chlamydomonadales;

4 AEMALACTOSH 15
 DB 335 AEMALACTOSH 346
 RESULT 12
 PRIR:ORENTI STANDARD: PRT: 630 AA.
 ID PRIR:ORENTI
 AC 01-OCT-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS Oreochromis niloticus (Nile tilapia) (Otilapia niloticus).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei;
 CC Clupeiformes; Clupeidae; Clupeinae; Clupeini; Clupeinae; Clupeidae;
 CC NCBI_TaxID=8128.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney.
 RX MEDLINE=55320210; PubMed=7597076;
 RA Sandra O., Som P., de Luca A., Prunet P., Bedy M., Kelly P.A.;
 RL Proc Natl Acad Sci U S A. 92:6037-6041(1995)
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A FIBROBLASTIN TYPE III-LIKE DOMAINS.
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 CC EMBL, L34723; AAA98997.1; -
 DR HSP: P16471; IBP3.
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR01777; FN.II.
 DR InterPro: IPR003528; Hematopo_rctpror_L.FI.
 DR Pfam: PF00041; En3. 2
 DR SMART: SM00061; F83. 2
 DR PROSITE: PS00108; Glycoprotein; Glycoprotein; Signal; Repeat.
 DR KX Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 630
 FT DOMAIN 24 234
 FT TRANSMEM 235 258
 FT DOMAIN 259 630
 FT DOMAIN 124 223
 FT DISULFID 137 47
 FT DISULFID 76 87
 FT CARBOHYD 92 92
 FT CARBOHYD 101 101
 SEQUENCE 630 AA; 70810 MW; AA515633012979D CRC64;

Query Match 46.9%; Score 38; DB 1; Length 630;
 Best Local Similarity 69.2%; Pct. No. 44;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 2 YEENALACTVSD 14
 DB 104 YVARNALACTVSD 116

RESULT 13
 YPK1 YEAST
 ID YPK1 YEAST STANDARD: PRT: 680 AA.
 AC P12688;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-JUN-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE YPK1 (EC 2.7.1.1).
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94090805; PubMed=2850145;
 RX "Isolation of a yeast protein kinase gene by screening with a
 RT mammalian protein kinase cDNA."
 RL DNA 7:469-474(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rad M.R., Xu G., Kirschner L., Fritz C., Keuchel H., Hollenberg C.P.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RP DISCUSSION OF SOURCE.
 RX MEDLINE=93173125; PubMed=8437590;
 RA Chen P.C., Lee K.S., Levin D.E.;
 RL Mol. Gen. Genet. 236:443-447(1993)
 CC -1- FUNCTION: PLAYS AN ESSENTIAL ROLE IN THE PROLIFERATION OF YEAST
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- RAC SUBFAMILY: STRONGEST TO YPK2.
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 CC EMBL, M21307; AAA34880.1; -
 DR EMBL, Z28126; CA81967.1; -
 DR PIR: S37955; S37955.
 DR SCOP: S0001609; YPK1.
 DR InterPro: IPR000719; Ser_thr_kin_actate.
 DR InterPro: IPR00290; Ser_thr_kin_actate.
 DR Pfam: PF00043; Kinase_C.1.
 DR SMART: SM00433; STK. 1.
 DR PROSITE: PS00107; PROTEIN KINASE, DOM. 1.
 DR PROSITE: PS00108; PROTEIN KINASE, STM. 1.
 DR PROSITE: PS50011; PROTEIN KINASE, DOM. 1.
 KM Transferase; Serine/threonine-protein kinase.
 FT DOMAIN 347 602
 FT NP_BIND 353 361
 FT BINDING 362 370
 FT BINDING 476 476
 FT BINDING 476 476
 FT CONFLICT 201 201
 FT CONFLICT 553 553
 SEQUENCE 680 AA; 76479 MW; 00112BB8A49CD2B5 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 680;
 Best Local Similarity 41.5%; Pct. No. 48;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 WVEASNALGV 11
 I: : :
 DB 318 WIRNLSMIRLTKH 128

RESULT 14
 DPOL_BPT3 STANDARD PRT: 704 AA.
 AC P20311:
 01-FEB-1991 (rel. 17, Created)
 01-FEB-1991 (rel. 17, Last sequence update)
 01-FEB-1991 (rel. 30, Last annotation update)
 DNA POLYMERASE (EC 2.7.7.7).
 OS Bacteriophage T3.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae;
 NCBI_TaxID=10759;
 RM SOURCE FROM N.A.
 RX MEDLINE=90131923; PubMed=2614843;
 RC STRAIN=HRTA;
 FT Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.:
 Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.;
 J. Mol. Biol. 210:687-701(1989).
 CC -1- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
 ALSO HAS 3'-5' EXONUCLEASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: N-DONKINUCLEOSIDE TRIPHOSPHATE -
 N PYROPHOSPHATE + DNA(N)
 CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS. ONE IS ENCODED BY THE PHAGE AND
 THE OTHER IS ENCODED BY THE MOST THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
 CC
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 CC
 CC EMBL: L3691; J06655; J06656;
 DR EMBL: J06655; J06656;
 DR EMBL: J06655; J06656;
 DR HSP: P00581; I177P;
 DR Interpro: IPR001096; DNA_POL_A.
 DR Pfam: PF00476; DNA_POL_A.1.
 DR SMART: SM00482; POLAC.1.
 DR PROSITE: PS00447; DNA_POLYMERASE.A.1.
 DR Transferrase: DNA-directed DNA polymerase; DNA replication;
 DR Nucleic acid binding; Nucleic acid binding;
 DR SOURCE: 704 AA; 79585 MW; D69DBD99AC1324 CIRC64;

Query Match 46.9%; Score 38; DB 1; Length 704;
 Best Local Similarity 57.1%; Pred.No. 50;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 WVEASNALGV 15
 I: : :
 DB 6 IERNLLEKVTSH 19

RESULT 15
 NIA_PETRY STANDARD PRT: 909 AA.
 AC P36859:
 01-JUN-1994 (rel. 29, Created)
 01-JUN-1994 (rel. 29, Last sequence update)
 01-OCT-1994 (rel. 30, Last annotation update)
 DE NITRATE REDUCTASE (EC 1.6.6.1) (NR).
 GN NIA.
 OS Petunia hybrida (Petunia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
 OC NCBI_TaxID=4102;
 RM
 RM SOURCE FROM N.A.
 RX MEDLINE=9329281; PubMed=8514183;
 RC STRAIN=CV; TIRL13; TISSUE=leaf;
 RA Salomabar M., Ha D.B.D.;
 FT *Analysis of the petunia nitrate reductase apoenzyme-encoding gene: a
 first step for sequence modification analysis.*;
 RL Gene 128:147-154(1993).
 CC -1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
 STEP OF NITRATE ASSIMILATION. IT CATALYZES THE REDUCTION OF NITRATE
 CC -1- CATALYTIC ACTIVITY: NADH + NITRATE -> NAD(+) + NITRITE + H(2)O.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- RYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 BY THE CIRCADIAN RHYTHM.
 CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION 2 HOURS AFTER SUNRISE. LOW
 CC EXPRESSION FOUND 2 HOURS BEFORE AND 8 HOURS AFTER SUNRISE.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
 CC -1- C-TERMINAL DOMAIN.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL collaboration -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L13691; AAA33713.1; -
 DR EMBL: J06655; J06656;
 DR HSP: P17571; 2CND;
 DR Interpro: IPR001199; Cyt_B5.
 DR Interpro: IPR001834; B6K-oxidoreductase.
 DR Interpro: IPR001433; Oxidoreductase.
 DR Pfam: PF009070; Cyt_reductase.1.ND.
 DR Pfam: PF00173; heme_1.1.
 DR Pfam: PF00175; oxidoreduct_fad.1.
 DR Pfam: PF00174; cytochromeB5.1.
 DR PRINTS: PR00163; CYTOCHROME_B5.
 DR PRINTS: PR00171; FPKR.
 DR PRINTS: PR00172; CYTOCHROME_B5.
 DR PRINTS: PR00407; HEMOPROTEIN.
 DR PROSITE: PS00191; CYTOCHROME_B5.1.1.
 DR PROSITE: PS00255; CYTOCHROME_B5.2.1.
 DR PROSITE: PS00559; MOLYBDOPTEIN_EUK.ND;
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 DR Nitrate assimilation; Multigene family.
 FT METAL: 187; 187; MOLYBDENUM-PTERIN (POTENTIAL);
 FT METAL: 426; 426; HEME IRON;
 FT DISULFID: 426; 426; HEME IRON;
 FT BINDING: 570; 570; HEME IRON;
 FT BINDING: 593; 593; HEME IRON;
 FT BINDING: 593; 593; HEME IRON;
 OS SOURCE: 909 AA; 102376 MW; 50207066B5E706 CIRC64;

Query Match 46.9%; Score 38; DB 1; Length 909;
 Best Local Similarity 57.3%; Pred.No. 6;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 WVEASNALGV 15
 I: : :
 DB 100 WIRNLSMIRLTKH 114

Search completed: December 19, 2001, 16:26:19
Job time: 574 sec

Genome version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:26 ; Search time 157.32 seconds
(without alignments)
13.947 Million cell updates/sec

Title: US-09-202-104a-9
Perfect score: 81
Sequence: 1 WEAENALGKVTSDH 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	329	4	090u41
2	65	80.2	918	13	09w609
3	47	58.0	422	4	075462
4	47	58.0	422	4	09uh5
5	47	58.0	422	11	09uhm8
6	43	54.3	1038	3	09x16
7	43	54.3	1038	3	09x16
8	43	53.1	666	5	016793
9	42	51.9	642	2	09jrk7
10	42	51.9	642	2	09jrk6
11	41	50.6	148	1	059138
12	41	50.6	264	6	028109
13	41	50.6	1035	3	028828
14	41	50.6	1035	3	028828
15	40	49.4	146	1	09v004
16	40	49.4	255	2	09s010
17	40	49.4	280	12	089642
18	40	49.4	552	2	096579
19	40	49.4	615	2	09zb96

ALIGNMENTS

20	39.5	48.8	686	2	09krl7	09rr17 delinococcus
21	39	48.1	161	2	09krl7	09krl7 vibrio chol
22	39	48.1	235	12	09pdx1	09dx1 cucurbit ye
23	39	48.1	235	12	09pdx2	09dx2 cucurbit ye
24	39	48.1	235	12	09pdx3	09dx3 cucurbit ye
25	39	48.1	235	12	09pdx4	09dx4 cucurbit ye
26	39	48.1	235	12	09pdx5	09dx5 cucurbit ye
27	39	48.1	235	12	09pdx6	09dx6 cucurbit ye
28	39	48.1	235	12	09pdx7	09dx7 cucurbit ye
29	39	48.1	235	12	09pdx8	09dx8 cucurbit ye
30	39	48.1	235	12	09pdx9	09dx9 cucurbit ye
31	39	48.1	235	12	09pdx10	09dx10 cucurbit ye
32	39	48.1	235	12	09pdx11	09dx11 cucurbit ye
33	39	48.1	235	12	09pdx12	09dx12 cucurbit ye
34	39	48.1	235	12	09pdx13	09dx13 cucurbit ye
35	39	48.1	235	12	09pdx14	09dx14 cucurbit ye
36	39	48.1	235	12	09pdx15	09dx15 cucurbit ye
37	39	48.1	235	12	09pdx16	09dx16 cucurbit ye
38	39	48.1	235	12	09pdx17	09dx17 cucurbit ye
39	39	48.1	235	12	09pdx18	09dx18 cucurbit ye
40	39	48.1	235	12	09pdx19	09dx19 cucurbit ye
41	39	48.1	235	12	09pdx20	09dx20 cucurbit ye
42	39	48.1	235	12	09pdx21	09dx21 cucurbit ye
43	39	48.1	235	12	09pdx22	09dx22 cucurbit ye
44	39	48.1	235	12	09pdx23	09dx23 cucurbit ye
45	39	48.1	235	12	09pdx24	09dx24 cucurbit ye

RESULT 1

09u041 PRELIMINARY; PRT; 329 AA.

AC 09u041; 01-JUN-2000 (TRENHARREL, 13, Created)

DT 01-JUN-2000 (TRENHARREL, 13, Last sequence update)

DE 01-JUN-2001 (TRENHARREL, 17, Last annotation update)

DE GP130 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE

DE FORM (GP130-RAP5).

GN GP130.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eumetazoa; Primates; Catarrhini; Hominoidea; Homo.

OC Hominidae; Homo; Homininae; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

OC Hominini; Hominini; Hominini; Hominini; Hominini;

Query Match 100.0%; Score 81; DB 4; Length 329;

Best Local Similarity 100.0%; Pred. No. 3e+06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WEAENALGKVTSDH 15

Db 197 WEAENALGKVTSDH 211

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RESULT 2
09M609 PRELIMINARY: PRT: 918 AA.
AC 09M609.
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE GLYCOPROTEIN 130 PRECURSOR.
GN Galus. gallus (chicken)
OS Gallus gallus (Chordata: Craniata: Vertebrata: Euteleostomi:
OC Archosauria: Aves: Neognathae: Galliformes, Phasianidae, Phasianinae:
CC Gallus.
NCBI_TaxID=9031.
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
RA Gelsen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
RL on gpl30 cytokine receptor signaling.";
RL Development 125:4791-4801(1998).
RM EMBL: A7011688; CMB2084.1; -.
DR HSSP: P40159; 1800; CRIA.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN.1.
RM Signal.
RT SIGNAL.
RN SEQUENCE 918 AA: 102495 MW; FE7625F3E3613EF CRC64;
SQ
Query Match 80.2%; Score 65; DB 13; Length 918;
Best Local Similarity 80.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 WEAEANAGKVTSD 15
Db 202 WEAEANAGKVTSD 216
RESULT 3
075462 PRELIMINARY: PRT: 422 AA.
AC 075462.
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Euteleostomi: Euteleostei, Primates, Catarrhini, Hominoidea, Homo.
NCBI_TaxID=9606.
RX [1]
RN SEQUENCE FROM N.A.
RA Elson G.C.A., Gaber P., Losberger P., Herren S., Gretenier D.,
RM Meunier L.N., Wells T.N.C., Kosco-Villhois M.H., Gauchat G.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the
RL Cytokine Type-01 (1998).
RN Immunol. 0:0-0(1998).
RX [2]
RN SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RL hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RM EMBL: AF073515; AF073515.1; -.
DR EMBL: AF073515; AF073515.1; -.

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DR HSSP: P40159; 1800;
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
RM Signal.
RT SIGNAL.
RN CHAIN 1 37
FT SIGNAL 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9CEFB01B64218 CRC64.
Query Match 58.0%; Score 47; DB 4; Length 422;
Best Local Similarity 64.3%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 WEAEANAGKVTSD 14
Db 210 WEAEANAGKVTSD 223
RESULT 4
09J0H5 PRELIMINARY: PRT: 422 AA.
AC 09J0H5.
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN CYTOS.
OS Homo sapiens (Human).
OC Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Euteleostomi: Euteleostei, Primates, Catarrhini, Hominoidea, Homo.
NCBI_TaxID=9606.
RX [1]
RN SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmsberg A.C., Gilbert T., Whitmore T.E.,
RM Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR HSSP: P40159; 1800; CRIA.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
RM Receptor.
RN SEQUENCE 422 AA; 46315 MW; 012C5F7A01B942BE CRC64;
SQ
Query Match 58.0%; Score 47; DB 4; Length 422;
Best Local Similarity 64.3%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 WEAEANAGKVTSD 14
Db 210 WEAEANAGKVTSD 223
RESULT 5
09J0H5 PRELIMINARY: PRT: 425 AA.
AC 09J0H5.
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CRF1 OR CRF3.
OS Mus musculus (Mouse).
OC Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Euteleostomi: Euteleostei, Primates, Catarrhini, Murinae, Mus.
NCBI_TaxID=10090.
RX [1]
RN SEQUENCE FROM N.A.
RA Hiroshima T., Iwama A., Nakamura Y., Nakachi H.;

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100

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:02 ; Search time 78.52 seconds
(without alignments)
4.299 Million cell updates/sec

Title: US-09-202-104a-9
Perfect score: 81 WYBENALCKVTSKH 15
Sequence: BLOSUM62
Scoring table: Gapop 10.0, Gapect 0.5

Searched: 212352 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212352

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents.AA:*
1: /cgn2.5/p/codata/2/1aa/5A.COMB.pep:*
2: /cgn2.5/p/codata/2/1aa/5B.COMB.pep:*
3: /cgn2.5/p/codata/2/1aa/5A.COMB.pep:*
4: /cgn2.5/p/codata/2/1aa/5B.COMB.pep:*
5: /cgn2.5/p/codata/2/1aa/5A.COMB.pep:*
6: /cgn2.5/p/codata/2/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	81	100.0	488	2	US-09-599-455B-5
2	81	100.0	488	4	US-09-069-781B-5
3	81	100.0	572	2	US-08-419-652-5
4	81	100.0	658	2	US-08-925-558-4
5	81	100.0	708	1	US-07-797-556-2
6	81	100.0	708	1	US-08-388-881-2
7	81	100.0	708	1	US-08-388-881-2
8	81	100.0	708	2	US-09-059-099-2
9	81	100.0	708	2	US-09-058-264-2
10	81	100.0	708	5	PCT-US95-06530-2
11	81	100.0	918	2	US-08-825-558-6
12	47	58.0	303	4	US-09-071-224-21
13	47	58.0	303	4	US-09-071-224-23
14	47	58.0	385	4	US-09-071-224-19
15	47	58.0	385	4	US-09-071-224-10
16	47	58.0	385	4	US-09-071-224-10
17	47	58.0	389	4	US-09-071-224-22
18	47	58.0	389	4	US-09-071-224-22
19	47	58.0	389	4	US-09-071-224-25
20	47	58.0	389	4	US-09-071-224-26
21	47	58.0	389	4	US-09-071-224-29
22	47	58.0	389	4	US-09-071-224-29
23	47	58.0	389	4	US-09-071-224-30
24	47	58.0	389	4	US-09-071-224-30
25	47	58.0	392	4	US-09-012-072-18
26	47	58.0	405	3	US-09-012-072-2
27	47	58.0	405	4	US-09-120-601-2

28	47	58.0	422	4	US-09-071-224-2	Sequence 2, App1
29	47	58.0	425	4	US-09-071-224-4	Sequence 4, App1
30	47	58.0	425	4	US-09-071-224-6	Sequence 6, App1
31	47	58.0	434	3	US-09-072-072-4	Sequence 4, App1
32	47	58.0	434	3	US-09-120-601-4	Sequence 4, App1
33	47	58.0	434	3	US-09-120-601-4	Sequence 4, App1
34	46	56.8	602	2	US-08-419-652-6	Sequence 6, App1
35	46	56.8	771	1	US-07-923-976-6	Sequence 6, App1
36	46	56.8	783	6	5422248-2	Patent No. 5422248
37	46	56.8	836	1	US-07-923-976-4	Sequence 4, App1
38	46	56.8	863	1	US-07-923-976-4	Sequence 4, App1
39	45	55.6	389	4	US-09-071-224-27	Sequence 27, App1
40	45	55.6	389	4	US-09-071-224-27	Sequence 27, App1
41	44.5	54.9	831	2	US-08-825-558-3	Sequence 3, App1
42	40	49.4	1462	3	US-07-792-600-31	Sequence 31, App1
43	40	49.4	1462	3	US-09-157-021-31	Sequence 31, App1
44	40	49.4	1462	3	US-09-156-842-31	Sequence 31, App1
45	36	44.4	35	4	US-08-810-009-19	Sequence 19, App1

ALIGNMENTS

US-09-599-455B-5
Sequence 5, Application US/08599455B
Patent No. 597821
GENERAL INFORMATION:
INVENTOR: Richard L. A.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: GENES 2.0/Genious Version 2.0
CURRENT APPLICATION NUMBER: US/08/599/455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 13-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
FIRM: Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455a-5

Query Match 100.0%; Score 81; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 9,9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEAEANALGKVTSDH 15
|||||
DB 168 WEAEANALGKVTSDH 162

RESULT 2

US-09-069-781b-5
Sequence 5, Application US/09069781b
Patent No. 5287972
GENERAL INFORMATION:
APPLICANT: Watson, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTED: For Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 25-APRIL-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/559,455
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/583,153
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkington, P.D., Anita L.
REFERENCE/DOCKET NUMBER: 0733/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781b-5

Query Match 100.0%; Score 81; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 9,9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEAEANALGKVTSDH 15
|||||
DB 168 WEAEANALGKVTSDH 162

RESULT 3

US-08-419-652-5
Sequence 5, Application US/08419652
Patent No. 5810072
GENERAL INFORMATION:
APPLICANT: Chu, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1995
APPLICATION NUMBER: US/08/419,652
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
APPLICATION NUMBER: US 08/094,713
ATTORNEY/AGENT INFORMATION:
NAME: Kees, Niam
REFERENCE/DOCKET NUMBER: 32142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 572
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..572
OTHER INFORMATION:
OTHER INFORMATION: 742 of human sp130.
US-08-419-652-5

Query Match 100.0%; Score 81; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 1,2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEAEANALGKVTSDH 15
|||||
DB 74 WEAEANALGKVTSDH 86


```

RESULT 4
US-08-825-558-4
: Sequence 4, Application US/0882558
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS: STEPHEN K. SMITH, JR.
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/825,558
: FILING DATE: 19-MAR-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0623_0530001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-825-558-4

Query Match
US-08-825-558-4 Similarity 100.0% Score 81; DB 2; Length 658;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/797,556
: FILING DATE: 19911122
: CLASSIFICATION: 404
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: TELEFAX: 206-587-0606
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 708 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: Protein
: US-07-797-556-2

```

```

Query Match
US-08-308-881-2 Similarity 100.0% Score 81; DB 1; Length 708;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211
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```

```

RESULT 5
US-07-797-556-2
: Sequence 2, Application US/07797556
: Patent No. 5265222
: GENERAL INFORMATION:
: APPLICANT: Gaeting, David P.
: TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/797,556
: FILING DATE: 19911122
: CLASSIFICATION: 404
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 231-0644
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-308-881-2

```

Query Match 100.0%: Score 81; DB 1; Length 708;
Best Local Similarity 100.0%: Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WVEENALGKVTSDH 15
Db 197 WVEENALGKVTSDH 211

RESULT 7

US-09-058-263-2
Sequence 2, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
TELEPHONE: (206) 587-0430
FILING DATE: US/09/058,263
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
FAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-263-2

Query Match 100.0%: Score 81; DB 2; Length 708;
Best Local Similarity 100.0%: Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WVEENALGKVTSDH 15
Db 197 WVEENALGKVTSDH 211

RESULT 8

US-09-059-099-2
Sequence 2, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
TELEPHONE: (206) 587-0430
FILING DATE: US/09/059,099
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
FAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%: Score 81; DB 2; Length 708;
Best Local Similarity 100.0%: Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WVEENALGKVTSDH 15
Db 197 WVEENALGKVTSDH 211

RESULT 9

US-09-058-264-2
Sequence 2, Application US/09058264
Patent No. 6010886
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
TELEPHONE: (206) 587-0430
FILING DATE: US/09/058,264

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
PUBLICATION NUMBER: US/08/249,553
PILIND DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
FAX: (206) 233-0644
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-056-264-2

Query Match
Best Local Similarity 100.0%; Score 81; DB 3; Length 708;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

```

```

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match
Best Local Similarity 100.0%; Score 81; DB 5; Length 708;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

RESULT 11
US-08-825-558-6
Sequence 6, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, STEPHEN K.
REGISTRATION NUMBER: 32,172
TELEPHONE: (202) 371-2600
FAX: (202) 371-2600
TITLE OF INVENTION: CD 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 0623,0530001
TELEPHONE: (408) 371-2600
FAX: (408) 371-2600
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS:
STREET:
CITY:
STATE:
COUNTRY:
ZIP:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/249,553
FILING DATE: 12-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 09-SEP-1994
PUBLICATION NUMBER: US/08/249,553
PILIND DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
FAX: (206) 233-0644
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 708 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-825-558-6

Query Match
Best Local Similarity 100.0%; Score 81; DB 2; Length 918;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

RESULT 12
US-09-071-224-21
Sequence 21, Application US/09071224
Patent No. 6271443
GENERAL INFORMATION:
APPLICANT: LOK, SI
ATTORNEY/AGENT INFORMATION:
NAME: Presnell, Scott R.
REGISTRATION NUMBER: 32,172
TELEPHONE: (206) 587-0430
FAX: (206) 233-0644
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 708 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-09-071-224-21

```

```

APPLICANT: Gilbert, Teresa
APPLICANT: Postner, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Zymogenetics
Street: 1201 Eastlake Ave East
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-21

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Query Match 58.0% Score 47: DB 4: Length 303:
Best Local Similarity 64.3%, Pred. No. 0.74:
Matches 9: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
QY 1 WVEENNALQKVTSD 14
DB 173 WVEENNLGASND 186

```

```

RESULT 13
US-09-071-224-23
Sequence 23: Application US/09071224
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jellmeberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Postner, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Zymogenetics
Street: 1201 Eastlake Ave East
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-23

```

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Query Match 58.0% Score 47: DB 4: Length 303:
Best Local Similarity 64.3%, Pred. No. 0.74:
Matches 9: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
QY 1 WVEENNALQKVTSD 14
DB 173 WVEENNLGASND 186

```

```

RESULT 14
US-09-071-224-19
Sequence 19: Application US/09071224
GENERAL INFORMATION:
PATENT NO. 6271343
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jellmeberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Postner, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Zymogenetics
Street: 1201 Eastlake Ave East
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:

```

NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 385 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-071-224-19

Query Match 58.0%; Score 47; DB 4; Length 385;
 Best Local Similarity 64.3%; Fred. No. 0.96;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 WVEARNALGKVTSD 14
 |||||
 Db 173 WVEATNRRLGSARSD 186

RESULT 15
 US-09-071-224-20
 Sequence 20, Application US/09071224
 Patent No. 6271343
 GENERAL INFORMATION:
 APPLICANT: Lok, SI
 APPLICANT: presnell, Scott R.
 APPLICANT: Jelmberg, Anna C.
 APPLICANT: Gilibert, Teresa
 APPLICANT: Jelmberg, Anna C.
 APPLICANT: Adams, Robyn L.
 APPLICANT: Lehner, Joyce M.
 TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: zymogenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS Windows Version 2.0
 SOFTWARE: ZCYTORS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,224
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 385 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-09-071-224-20
 Query Match 58.0%; Score 47; DB 4; Length 385;
 Best Local Similarity 64.3%; Fred. No. 0.96;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 WVEARNALGKVTSD 14
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 Db 173 WVEATNRRLGSARSD 186

Search completed: December 19, 2001, 16:21:02
 Job time: 407 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using SW model

Run on: December 19, 2001, 16:19:36 ; Search time 170.68 Seconds
(without alignments) 7.378 Million cell updates/sec

Title: US-09-202-104a-10
Sequence: 1 PYKWKRPNPINLSTN 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 52463 seqs, 74071390 residues

Total number of hits satisfying chosen parameters: 52463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

- A. Genesec 1101.*
- 1: /SID8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
 - 2: /SID8/gcgdata/geneseq/geneseqp/AA1981.DAT.*
 - 3: /SID8/gcgdata/geneseq/geneseqp/AA1982.DAT.*
 - 4: /SID8/gcgdata/geneseq/geneseqp/AA1983.DAT.*
 - 5: /SID8/gcgdata/geneseq/geneseqp/AA1984.DAT.*
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 - 7: /SID8/gcgdata/geneseq/geneseqp/AA1986.DAT.*
 - 8: /SID8/gcgdata/geneseq/geneseqp/AA1987.DAT.*
 - 9: /SID8/gcgdata/geneseq/geneseqp/AA1988.DAT.*
 - 10: /SID8/gcgdata/geneseq/geneseqp/AA1989.DAT.*
 - 11: /SID8/gcgdata/geneseq/geneseqp/AA1990.DAT.*
 - 12: /SID8/gcgdata/geneseq/geneseqp/AA1991.DAT.*
 - 13: /SID8/gcgdata/geneseq/geneseqp/AA1992.DAT.*
 - 14: /SID8/gcgdata/geneseq/geneseqp/AA1993.DAT.*
 - 15: /SID8/gcgdata/geneseq/geneseqp/AA1994.DAT.*
 - 16: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT.*
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 - 18: /SID8/gcgdata/geneseq/geneseqp/AA1997.DAT.*
 - 19: /SID8/gcgdata/geneseq/geneseqp/AA1998.DAT.*
 - 20: /SID8/gcgdata/geneseq/geneseqp/AA1999.DAT.*
 - 21: /SID8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
 - 22: /SID8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
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2	95	100.0	24	AAW2210			Human interleukin-
3	95	100.0	180	17	AAW0404		Interleukin-6 anta
4	95	100.0	329	20	AAW17859		Rheumatoid arthrit
5	95	100.0	323	20	AAW07959		Human gp130-delta
6	95	100.0	656	17	AAW34758		Human gp130-delta
7	95	100.0	656	17	AAW34758		Human gp130-delta
8	95	100.0	708	14	AAW37804		Human gp130 N-term
9	95	100.0	708	14	AAW37804		Human gp130 N-term
10	95	100.0	727	21	AAW921592		Human gp130-kappa
11	95	100.0	738	21	AAW921594		Human gp130-j-kapp

12	95	100.0	859	20	AAW0796		Human gp130-Fc-His
13	95	100.0	859	21	AAW92184		Human gp130-Fc-His
14	95	100.0	918	12	AAW10545		Recombinant human
15	95	100.0	918	15	AAW6233		Human soluble glyco
16	95	100.0	918	17	AAW44558		Human gp130 protol
17	95	100.0	918	21	AAW44558		Human gp130 protol
18	95	100.0	951	20	AAW07968		Human gp130-C-gamm
19	95	100.0	951	21	AAW92186		Human gp130-C-gamm
20	95	100.0	951	21	AAW92186		Human gp130-C-gamm
21	95	100.0	1158	21	AAW92187		Human gp130-j-kapp
22	95	100.0	1158	21	AAW92205		Fusion polypeptide
23	68	71.6	924	22	AAW88339		Human Interleukin-
24	68	71.6	924	22	AAW88339		Human Interleukin-
25	68	71.6	917	22	AAW55074		Human gp130 protol
26	52	54.7	24	22	AAW88337		Human Interleukin-
27	48.5	51.1	361	22	AAW88337		s. epidermidis ope
28	47	49.5	400	16	AAW71932		I-branching enzyme
29	47	49.5	400	17	AAW92474		Beta-1,6-N-acetylgl
30	47	49.5	400	19	AAW65658		Full length amino
31	47	49.5	400	19	AAW67184		Human beta-1,6-N-A
32	46	48.4	266	22	AAW90578		Human beta-1,6-N-A
33	46	48.4	266	22	AAW90578		Human beta-1,6-N-A
34	46	48.4	426	18	AAW05822		Human Interleukin-
35	46	48.4	427	18	AAW24973		Human Interleukin-
36	46	48.4	427	22	AAW19807		Human Interleukin-
37	46	48.4	427	22	AAW19808		Human Interleukin-
38	46	48.4	784	21	AAW92207		Human Interleukin-
39	46	48.4	784	21	AAW92207		Human Interleukin-
40	46	48.4	784	21	AAW92207		Human Interleukin-
41	45	47.4	69	22	AAW14436		Human novel proteol
42	45	47.4	5701	22	AAW05338		Human beta #410 (cnc
43	45	47.4	26926	22	AAW05338		Human beta #410 (cnc
44	45	47.4	626	18	AAW16398		Human neuron-deciv
45	45.3	18	19	AAW6395			Cationic peptide a

ALIGNMENTS

RESULT	ID	AAW2210	standard: peptide: 17 AA.
1	AAW2210		
09-JUN-1998	(first entry)		
Interleukin-6 antagonist peptide.			
Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma; acquired immune deficiency syndrome-related lymphoma; immune response; rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy; Alzheimer's disease.			
Synthetic.			
OS Homo sapiens.			
XX MO9748728-A1.			
XX 24-DEC-1997.			
XX 19-JUN-1997.			
XX 20-JUN-1996.			
PR 96EP-0201720.			
PR 97MO-NL00345.			
PA (KOSTER) KOSTER H W.			
XX Hoebe KIN. Van Leengoed LMG.			
XX WPI: 1998-063080/06.			
DR New peptide(s) with interleukin-6 agonist or antagonist activity -			
XX useful for treatment, prevention and diagnosis of IL-6 associated			
PT			

FH Key Location/Qualifiers
 FE Protein 1..330
 FE Peptide 216-232 gp130
 FT Peptide 331-332
 FT /note= "Ser-Gly bridge"
 PN W0200018932-A2.
 PM 06-APR-2000.
 PP 22-SEP-1999; 99NO-US22045.
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0319442.
 PA (REGC-) REGENERON PHARM INC.
 PA Stahl M, Yancopoulos GP;
 PM WPI: 2000-293165/75.
 DR WPI: 2000-293165/75.
 XX
 XX Isolated nucleic acid molecule for treating cytokine-related diseases
 FT or disorders encodes a fusion polypeptide capable of binding a cytokine
 FT to form a nonfunctional complex
 PM
 PM Example 4; Fig 10; 152pp: English.
 XX
 XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC intermediate being a non-functional complex.
 CC (a) a first beta signal transducing component (beta-1) that acts as a
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (aR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (cellary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC use of a non-functional intermediate complex, in particular, in
 CC the presence of a ligand, its alpha receptor and its beta-1 receptor
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining
 CC components of their receptors and the alpha specifically determining
 CC the resultant heterodimers, function as high-affinity traps rendering
 CC the resultant heterodimers, function as high-affinity traps rendering
 CC the native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC
 SQ Sequence 332 AA:
 QY 1 PYYKVKRPNPNNLSYIN 17
 DB 216 PYYKVKRPNPNNLSYIN 232
 QY Query Match 100.0%; Score 95; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2, 5e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Human gp130 splice variant.
 XX Gp130; transmembrane domain; growth factor antagonist;
 XX embryo preimplantation; in vitro fertilisation.
 XX
 XX Homo sapiens.
 OS
 EN W09609382-A1.
 XX 28-MAR-1996.
 XX
 XX 21-SEP-1995; 95WO-GB02243.
 PF
 PR 21-SEP-1994; 94GB-0019021.
 XX
 XX (ISTF) ARS APPLIED RES SYST HOLDING NV.
 PA Dellow KA, Sharkey A, Smith SK;
 PM WPI: 1996-188444/19.
 DR N-PSDB: AAT14602.
 XX
 XX New splice variant of gp130 lacking the trans-membrane domain
 PF useful as an antagonist for growth factors esp. for ensuring correct
 FT development of pre-implantation embryos
 PM
 PM Example 2; Fig 1; 33pp: English.
 XX
 XX A novel, soluble splice variant (AA94576) of human gp130 corresponds
 CC to amino acids 1-613 of native gp130 (AA75368) but has a novel
 CC C-terminal sequence (AA94575) from amino acid 614 onwards.
 CC The splice variant lacks a transmembrane region. It was initially
 CC used as a growth factor antagonist in the development of growth
 CC factors. The splice variant antagonises the action of growth
 CC factors, e.g. interleukin-6, leukaemia inhibitory factor,
 CC oncostatin M and interleukin-11, and can be used to ensure correct
 CC development of preimplantation embryos, partic. for in vitro
 CC fertilisation.
 CC
 SQ Sequence 658 AA:
 QY 1 PYYKVKRPNPNNLSYIN 17
 DB 216 PYYKVKRPNPNNLSYIN 232
 QY Query Match 100.0%; Score 95; DB 17; Length 658;
 Best Local Similarity 100.0%; Pred. No. 5, 3e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PYYKVKRPNPNNLSYIN 17
 DB 216 PYYKVKRPNPNNLSYIN 232
 QY Query Match 100.0%; Score 95; DB 17; Length 708 PA.
 ID AA937804
 XX AA937804:
 XX
 XX 01-OCT-1993 (first entry)
 DT
 XX Human gp130 N-terminal fragment.
 DE
 XX
 XX Oncostatin M; leukaemia inhibitory factor; receptor; PCR; fusion;
 KM LIP-R; gp130; linker.
 XX
 XX Synthetic.
 OS
 EN
 XX
 XX Key Location/Qualifiers
 FE Peptide 1..22
 FT /label= sig-peptide
 FE Protein 23..708
 FE /label= mat-protein
 FE 23..619
 FE /label= extracellular_domain

FT	Peptide	1..22	/note="Signal peptide"
FT	Peptide	23..708	/note="N-terminal fragment of mature gp130"
FT	Modified-site	21..23	/note="glycosylation site"
FT	Modified-site	60..63	/note="glycosylation site"
FT	Modified-site	109..111	/note="glycosylation site"
FT	Modified-site	135..137	/note="glycosylation site"
FT	Cleavage-site	133..134	/note="glycosylation site"
FT	Modified-site	224..226	/note="glycosylation site"
FT	Modified-site	357..359	/note="glycosylation site"
FT	Modified-site	361..363	/note="glycosylation site"
FT	Modified-site	367..370	/note="glycosylation site"
FT	Modified-site	531..533	/note="glycosylation site"
FT	Modified-site	542..544	/note="glycosylation site"
FT	Cleavage-site	621..622	/note="glycosylation site"
PD	07-DEC-1995.		
PD			
PP	22-MAY-1995;	95NO-0506530.	
PR	12-SEP-1994;	9405-0308881.	
PR	26-MAR-1994;	9405-0249553.	
PA	(IMV) IMVINCX CORP.		
PI	Cosman BJ, Mostley B;		
DR	WPI; 1996-030570/03.		
DR	N-FSDB; AAO74081.		
PT	Hetero-oligomeric receptor proteins comprising OSM-R-beta and gp 130 -		
PT	bind oncostatin M and are used in inhibiting biological activities		
PT	mediated by oncostatin M		
XX			
PS	Claim 1; Page 35-38; 60pp: English.		
XX			
XX	This sequence represents an N-terminal fragment of gp130 obtained from		
XX	the C-terminus of gp130. The amino acid sequence is shown in a single		
XX	chain polypeptide cytochrome oncostatin M regulates the growth of		
XX	certain tumour derived and normal cell lines. This receptor protein, and		
XX	the oncostatin M receptor-beta chain (see AAB5912) sequence can be		
XX	covalently joined, to give a heterodimeric receptor protein capable of		
XX	binding to oncostatin M. The receptors can also comprise fusion		
XX	polypeptides, where an antibody Fe region is joined to the C-terminus of		
XX	each of the polypeptides. The amino acid sequence of the antibody Fe region		
XX	is shown in a single chain polypeptide. The amino acid sequence of the		
XX	heterodimeric receptors can be used to inhibit biological activities		
XX	mediated by oncostatin M. The advantage with using the heterodimeric		
XX	receptors is that they bind to oncostatin M at greater levels than gp130		
XX	does alone.		
XX			
XX	Sequence 708 AA:		
XX			
XX	Query Match	100.0%; Score 95; DB 17; Length 708;	
XX	Best Local Similarity	100.0%; Pred. No. 5,7e-06;	
XX	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

XX	Economides A., Stahl N., Yancopoulos GD;
PI	
DR	WPI; 1999-044669/04.
XX	
XX	Cytokine antagonists - comprising extracellular domains of
PT	specifically determining and signal-transducing components of
PT	cytokine receptor
XX	
XX	Example 3: Fig 4; 46pp; English.
CC	The present sequence represents the amino acid sequence of human
CC	gp130-Fc-His6. The protein is used in the course of the invention. The
CC	specification describes cytokine antagonists comprising only the
CC	extracellular domain of gp130 or gp130-Fc-His6, which are composed of
CC	the cytokine receptor and the extracellular domain of a
CC	signal-transducing component of the cytokine receptor. The cytokine
CC	is an interleukin (IL)-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC	granulocyte macrophage colony-stimulating factor (GM-CSF),
CC	gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC	antagonist is capable of binding the cytokine to form a nonfunctional
CC	complex. The compounds have therapeutic activity as cytokine antagonists
CC	and agonists of cytokines.
SQ	
Sequence	859 AA:
Query Match	100.0%; Score 95; DB 20; Length 859;
Best Local Similarity	100.0%; Pct. Id. = 76% 0;
Matches 17; Conserving	0; Mismatches 0; Indels 0; Gaps 0;
Yq	1 PYKKVKNPNNHLSVIN 17
Db	216 PVYKVKPPNPHLSEVIN 232
RESULT# 13	
ID	AAV92184 standard; protein; 859 AA.
XX	AAV92184;
AC	
DT	01-AUG-2000 (first entry)
XX	
XX	Human gp130-Fc-His6.
KM	gp130-Fc-His6; cytokine; antagonist; CNMF; receptor; fusion protein;
XX	cytostatic; immunomodulator; osteopethtic.
XX	Synthetic.
OS	Homo sapiens.
XX	
XX	Key location/Qualifiers
XX	Protein /label= gp130
FT	Peptide 1..22
FT	/label= signal-peptide
FT	Peptide 620..621
FT	/note= "ser-gly bridge"
FT	Disulfide-bond 632
FT	/note= "forms inter-chain disulfide bridge that
FT	link two FC domains"
FT	Disulfide-bond 633
FT	/note= "forms inter-chain disulfide bridge that
FT	link two FC domains"
FT	Protein 662..853
FT	/label= IgG1-FC-domain
FT	Peptide 854..859
XX	/label= histidine-tag
XX	
XX	WO200018937-A2.

```

FD      06-APR-2000 .
PE      22-SEP-1998;    99MO-US22045 .
PF      25-SEP-1998;    98US -0101858 .
PR      19-MAY-1999;    99US -0313942 .
PA      (RECE-) REGENERON PHARM INC.
PI      Stahl N, Yancopoulos GD;
PX      WPI: 2000-293165/25.
PY      Isolated nucleic acid molecule for treating cytokine-related diseases
PT      or disorders encodes a fusion polypeptide capable of binding a cytokine
PX      to form a nonfunctional complex
PS      Example 3: Fig 4: 152pp: English.
XX
XX      The invention concerns production of antagonists to any cytokine that
XX      can bind to any receptor, such as the interleukin-6 receptor, which is
XX      combined with the cytokine binds to first beta signal transducing component to
XX      form a non-functional intermediate which then binds to a second beta
XX      signal transducing component causing beta-receptor dimerization, the
XX      soluble alpha specifically determining component of the receptor
XX      (sR-alpha) and the extracellular domain of the beta-1 are combined to
XX      transducing component of the extracellular domain of the beta-1 are combined to
XX      form heterodimer (sR-alpha-beta-1) that act as antagonist to the
XX      receptor components are shared by cytokines such as the CNP regulatory
XX      neurotrophic factor) family of IL-6 antagonists, as they show that if, in
XX      the presence of a ligand, a non-functional intermediate complex,
XX      consisting of the ligand, its alpha receptor and its beta-1 receptor
XX      component, can be formed, it will effectively block the action of the
XX      native membrane receptors of the alpha and beta-1 receptors of heterodimers
XX      of the extracellular domains of the alpha and beta-1 receptors of heterodimers
XX      CC components of their receptors and the extracellular domain of gp130.
XX      CC The resultant heterodimers, function as high-affinity traps, rendering
XX      the cytokine inaccessible to form a signal transducing complex with the
XX      native membrane-bound forms of their receptor. The nucleic acids and
XX      polypeptides are useful for treating cytokine-related diseases or
XX      disorders such as osteoporosis and primary and secondary effects of
XX      cancer including multiple myeloma or cachexia.
XX
XX      Sequence      859 AA:
SQ
SQ      Query Match          100.0%; Score 95; DB 21; Length 859;
SQ      Best Local Similarity 100.0%; Pred. No. 7e-06;
SQ      Matches 17; ConservedActive 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 PYKWKPPHPPHSLVYN 17
OY      |||||||||
OY      216 PYYKYVPHPHSLVYN 232
OY      |||||||||
RESULT_14
NAI0545
AAKI0545 standard; Protein; 918 AA.
AC      AAKI0545;
DE      12-APR-1991 (first entry)
DE      Recombinant human gp130 protein.
DE      KX      Recombinant human gp130; interleukin-6; interleukin-6 receptor;
DE      KM      immunity; haematopoiesis, inflammation; therapy.
OS      XX      Homo sapiens.
EN      EP411946-A.

```

XX	PD	06-FEB-1991.
XX	PE	02-AUG-1990; 90EP-0308530.
XX	PR	31-MAY-1990; 90JP-0140069.
XX	PR	03-AUG-1989; 89JP-0200230.
XX	PA	(KISH/) KISHIMOTO T.
XX	PI	Kishimoto T;
XX	DR	WPI: 1991-038820/06.
XX	DS	N-PDB: AA010402.
PT	PX	Recombinant human gp130 protein - acts in the transmission of interleukin-6 signal for defence mechanisms
XX	XX	
XX	PS	Disclosure; fig 7; 3app; English.
CC	CC	This gp130 protein is produced using standard recombinant DNA methods (see AA010402), free from any other human protein. It participates in the transmembrane of the interleukin (IL)-6 signal, and therefore the proliferation and differentiation of an organism. It is important in an animals defence mechanisms, e.g. immunity, haematopoiesis and inflammation.
XX	XX	
SQ	Sequence	918 AA:
Query Match	100.0%;	Score 95; DB 12; Length 918;
Best Local Similarity	100.0%;	Pred. No. 7.6e-06;
Matches 17; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1 PYYKKRPMPHNSVSN 17 	
DQ	216 PYKKRPPHNPISVIN 232 	
RESULT 15		
AAR6233	ID AAR6233; standard; Protein; 918 AA.	
XX	AAAR6233;	
XX	XX	
DI	15-SEP-1994 (first entry)	
XX	DE Human soluble glycoprotein (gp) 130.	
XX	Glycoprotein; soluble; gp; gp130; antibody production; assay; immunochemical assay; detection; immunogen; transmembrane domain.	
OS	Homo sapiens.	
XX	JF06022786-A.	
PN	01-FEB-1994.	
XX	02-AUG-1991; 91JP-0217924.	
PE	02-AUG-1991; 91JP-0217924.	
PA	(KISH/) KISHIMOTO C.	
PA	(TOYU) TOSHIO CORP.	
XX	WPI: 1994-071006/09.	
XX	DR N-PDB: AA069311.	
PT	Preparation of recombinant soluble human gp 130 deriv - for use in the production of anti-gp 130 antibody for immunochemical assay	
XX	Claim 1; Figure 7; 13pp; Japanese.	

XX
 CC The soluble glycoprotein (gp) 130 can be used as an immunogen for
 CC the preparation of anti-gp130 antibody and as the standard substance
 CC for immunocemical assay of gp130. Soluble gp130 cDNA was prepared
 CC by reverse transcription-polymerase chain reaction (RT-PCR) using
 CC or transmembrane domain of the gp130 coding sequence or simply by
 CC eliminating the transmembrane domain.
 XX

SO Sequence 918 AA:

Query Match 100.0% Score 95; DB 15; Length 918;
 Identical Similarity 100.0%; Positives 7 de-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PYYKXKPNPNLSVIN 17
 |||||
 Db 216 PYYKXKPNPNLSVIN 232

Search completed: December 19, 2001, 16:19:37
 Job time: 362 sec

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Genome version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:41 ; Search time 88.82 seconds
(without alignments)
14,580 Million cell updates/sec

File: us-09-202-104a-10

Sequence: 1 PYKVKPNPNHLSVJN 17

Scoring table: BLOSUM62
Gapop 10.0, Capext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Database: PIR 68:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

Printed: No. is the number of results predicted by chance to have a
percentage of the total score of the residues being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	95	100.0	918	A4257	interleukin-6 signal transducing molecule gp130 - rat
2	75	78.9	918	A4257	interleukin-6 signal transducing molecule gp130 - rat
3	68	71.6	917	I49699	glycoprotein gp130 - human
4	47	49.5	225	T09564	extensin CPG15 pre
5	47	49.5	400	A46297	beta-1,6-N-acetylglucosaminidase
6	47	49.5	491	T07598	proline-rich prote
7	45	47.4	692	S64904	proline-rich prote
8	45	47.4	692	S64904	proline-rich prote
9	45	47.4	692	S64904	proline-rich prote
10	44	46.3	625	S71930	neuron-derived rec
11	44	46.3	625	S71930	neuron-derived rec
12	44	46.3	625	S71930	neuron-derived rec
13	44	46.3	625	S71930	neuron-derived rec
14	43.5	45.8	199	T27135	hypothetical prote
15	43	45.3	199	T27135	hypothetical prote
16	43	45.3	199	T27135	hypothetical prote
17	43	45.3	199	T27135	hypothetical prote
18	43	45.3	199	T27135	hypothetical prote
19	43	45.3	199	T27135	hypothetical prote
20	43	45.3	199	T27135	hypothetical prote
21	43	45.3	199	T27135	hypothetical prote
22	43	45.3	199	T27135	hypothetical prote
23	43	45.3	199	T27135	hypothetical prote
24	43	45.3	199	T27135	hypothetical prote
25	43	45.3	199	T27135	hypothetical prote
26	43	45.3	199	T27135	hypothetical prote
27	43	45.3	199	T27135	hypothetical prote
28	43	45.3	199	T27135	hypothetical prote
29	43	45.3	199	T27135	hypothetical prote

30	42	44.2	412	A41070	prolactin receptor
31	42	44.2	492	S49147	BRP-2 protein - hu
32	42	44.2	513	C84447	probable MKR9 DMA-
33	42	44.2	513	S20900	clonin mouse (ftr
34	42	44.2	513	S20900	clonin mouse (ftr
35	42	44.2	608	I53265	prolactin receptor
36	42	44.2	610	A34631	prolactin receptor
37	42	44.2	610	A34631	prolactin receptor
38	42	44.2	610	A34631	prolactin receptor
39	42	44.2	656	B96649	hypothetical prote
40	42	44.2	1049	T43020	hypothetical prote
41	42	44.2	1187	T25283	hypothetical prote
42	42	44.2	6805	S20901	clonin - rabbit (fr
43	42	44.2	6805	S20901	clonin - rabbit (fr
44	42	44.2	6805	S20901	clonin - rabbit (fr
45	42	44.2	6805	S20901	clonin - rabbit (fr

ALIGNMENTS

RESULT 1
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence, revision 12-Apr-1991 #text, change 28-Jul-2000
C:Accession: A36337
R:HB1, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; PMID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HTB>
A:Cross-references: GB:57230; NID:9186353; PID:AAA59155.1; PID:9186354
A:Genetic DB: I1657; GP130
A:Cross-references: GB:126725; OMIM:600694
A:Map position: 5q11-5q11
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
P:134-315/Domain: cytokine receptor homology <CRS>

Query Match 100.0% Score 95; DB 2; Length 918;
Best Local Similarity 100.0%; Print No. 6, 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYKVKPNPNHLSVJN 17
DB 216 PYKVKPNPNHLSVJN 232

RESULT 2
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence, revision 18-Nov-1994 #text, change 28-Jul-2000
C:Accession: A44257
R:Accession: A44257
Genomics 14, 566-572, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc
A:Reference number: A44257; PMID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <HTB>
A:Cross-references: OMIM:600694
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
P:134-315/Domain: cytokine receptor homology <CRS>


```

RESULT 10
S71930
neuron-derived receptor NOR-1 - human
C:Species: Homo sapiens (man)
C:Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998
A:Accession: S71930
A:Keywords: N.; Ito, M.; Tanabe, T.; Sasag, K.; Yamaguchi, K.; Miki, K.
A:Title: Structure, mapping and expression of a human NOR-1 gene, the third member of the
A:Reference number: S71930; MUID:96404972
A:Accession type: mRNA
A:Molecule type: mRNA
A:Residues: 1-625 <OHK>
A:Cross-references: EMBL:D78579
A:Note: DNA was also sequenced
A:Map position: 9q
C:Superfamily: probable hormone receptor N10, nuclear; erba transforming protein homolog
C:Keywords: DNA binding; receptor; zinc finger
F:290-544/Domain: erba transforming protein homolog <ERBA>
F:290-317/Domain: DNA binding [status predicted <DNA>]
F:292-312/Region: zinc finger CCCC motif
F:310-314/Region: P box finger CCCC motif
F:312-313/Region: D box
F:329-331/Region: D box
F:370-376/Region: A box

Query Match 46.3%; Score 44; DB 2; Length 625;
Best Local Similarity 54.3%; Pred. NO. 43;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVRKVPMPN 11
DB 189 PLFHKPSPN 199

RESULT 11
S71930
neurotrophin protein Y53C12B.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27136
R:Kestlav, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20316
A:Accession type: DNA
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-867 <MUL>
A:Cross-references: EMBL:Z59278; PIDN:CA316493.1; GSPDB:GN00020; CESP:Y53C12B.3a
A:Experimental source: clone Y53C12B
A:Gene: Y53C12B
A:Map position: 2
A:Introns: 100/3; 177/3; 218/1; 423/3; 714/2; 864/3

Query Match 46.3%; Score 44; DB 2; Length 867;
Best Local Similarity 58.3%; Pred. NO. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVRKVPMPN 12
DB 268 PVIOORPEPPN 279

RESULT 12
S72135
neurotrophin protein Y53C12B.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

```

```

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T27136
R:Kestlav, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20316
A:Accession type: DNA
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-871 <MUL>
A:Cross-references: EMBL:Z59278; PIDN:CA316492.1; GSPDB:GN00020; CESP:Y53C12B.3b
A:Experimental source: clone Y53C12B
A:Gene: CESP:Y53C12B.3b
A:Map position: 2
A:Introns: 100/3; 177/3; 218/1; 423/3; 717/2; 867/3

Query Match 46.3%; Score 44; DB 2; Length 871;
Best Local Similarity 58.3%; Pred. NO. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVRKVPMPN 12
DB 268 PVIOORPEPPN 279

RESULT 13
T07622
extensin homolog - soybean (fragment)
N:Alternate names: hydroxyproline-rich glycoprotein
C:Species: Glycine max (soybean)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
C:Accession: T07622
R:Y.H.; Nagao, R.T.; Bahk, J.D.; Cho, M.J.; Key, J.L.
Plant Physiol. 104:793-796, 1994
A:Title: Isolation and characterization of three soybean extensin cDNAs.
A:Reference number: Z16058; MUID:94211912
A:Accession: T07622
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-199 <OHK>
A:Cross-references: EMBL:U122029; NID:9347452; PIDN:AAA33970.1; PID:9347453
A:Experimental source: strain Wayne, seedling
C:Gene: HRC3
A:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: glycoprotein; hydroxyproline

Query Match 45.8%; Score 43.5; DB 2; Length 199;
Best Local Similarity 75.0%; Pred. NO. 14;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 PVRKVPMPN 11
DB 131 PVRKVPSPN 142

RESULT 14
S06675
apidaecin 1b precursor - honeybee
C:Species: Apis mellifera (honeybee)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Dec-1998
C:Accession: S06675
R:Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8:2387-2391, 1989
A:Title: Apidaecins: antibacterial peptides from honeybees.
A:Reference number: S05383; MUID:90005446
A:Accession: S06675
A:Molecule type: protein
A:Residues: 1-26 <CHS>
A:Cross-references: EMBL:U050516; status experimental <PRO>
F:9-26/Product: apidaecin 1b status experimental <ANT>

```

Query Match 45.3%; Score 43; DB 2; Length 26;
 Best Local Similarity 63.6%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PYWKVKNPPH 11
 ||| : |||
 DB 13 PYIIPQPPH 23

RESULT 15
 835331
 apIdacIn 22 precursor - honeybee
 C:Species: Apis mellifera (honeybee)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S35331
 R:Castels-Josson, K.; Capaci, T.; Castels, P.; Tempst, P.
 EMBL J. 12, 1569-1578, 1993
 A:Description: 151-residue precursor structure: a putative mechanism for amplification of the 15S ribosomal RNA.
 A:Accession: S35331
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 <CDS>
 A:Cross-references: EMBL:X72576; NID:9297064; PID:CA51168.1; PID:9297065
 C:Superfamily: procyelic acidic repetitive protein

Query Match 45.3%; Score 43; DB 2; Length 144;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PYWKVKNPPH 11
 ||| : |||
 DB 47 PYIIPQPPH 57

Search completed: December 19, 2001, 16:22:42
 Job time: 462 sec

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CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROX; NOTE-CD guide CD130 entry;
 CC WWW-<http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm>.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: M52230; AA59155.1; -
 CC EMBL: AB015706; BA478112.1; -
 CC PIR: A36337; A36337.
 CC PDB: 1HQJ; 26-ANG-98.
 CC MIM: 600694; -
 CC InterPro: IPR002995; CRIA.
 CC InterPro: IPR003526; RLITL.
 CC InterPro: IPR003529; Hematopo_receptor_L.F2.
 CC Pfam: PF00041; fn3; 3
 CC PRINTS: PRO0014; ENTPEPIT.
 CC SMART: SM00060; FN3; 3.
 CC PROSITE: PS01353; HEMATOPO_REC_L.F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Receptor: 3D structure Alternative splicing.
 CC STICK: 22
 CC CHAIN: 23 918
 CC FT DOMAIN 23 619 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC FT TRANSMEM 620 641 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 26 918 POTENTIAL.
 CC FT DOMAIN 124 322 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 124 322 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 325 423 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 424 517 FIBRONECTIN TYPE-III 3.
 CC FT DOMAIN 518 613 FIBRONECTIN TYPE-III 4.
 CC FT DOMAIN 725 755 FIBRONECTIN TYPE-III 5.
 CC FT DISULFED 28 54 SER-RICH.
 CC FT DISULFED 48 103
 CC FT DISULFED 124 164
 CC FT DISULFED 127 164
 CC FT DISULFED 174 164
 CC FT DISULFED 458 466
 CC FT CARBOHYD 43 43
 CC FT CARBOHYD 83 83
 CC FT CARBOHYD 131 131
 CC FT CARBOHYD 157 157
 CC FT CARBOHYD 227 227
 CC FT CARBOHYD 327 327
 CC FT CARBOHYD 383 383
 CC FT CARBOHYD 553 553
 CC FT CARBOHYD 564 564
 CC FT VARSPLIC 325 329
 CC FT VARSPLIC 330 918
 CC FT VARSPLIC 918 918
 CC SEQUENCE 918 AA; 103522 MW; D013F3672D01D053 CRC64;
 CC -----
 CC Query Match 100.0%; Score 95; DB 1; Length 918;
 CC Best Local Similarity 100.0%; Seed No. 2,4e-07;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC 0Y 1 PUYKAKPNPNHLSYIN 17
 CC DB 216 PUYKAKPNPNHLSYIN 232
 CC RESULT 2

IL6B_RAT
 ID IL6B_RAT STANDARD; PRT; 918 AA.
 NC 010108
 DE 01-FEB-1995 (Rel. 31, Created)
 DE 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6- β) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 NM IL6ST.
 OS Mammalia inaequale (Rat).
 OC Mammalia: Eutheria: Creatura: Vertebrata: Eucastorcomi:
 OC Mammalia: Eutheria: Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RK MEDLINE-93052397; PubMed-1427893;
 RK Wong M., Nesbitt J.B., Frances N.L., Fuller G.M.;
 RK Proc Natl Acad Sci USA 92:1447-1451 (1995).
 RL transducing molecule gp130.
 RL Genomics 14:666-672(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, ILF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
 CC -1- SUBUNIT: HETEROOLIGOMER OF SIMILARITY. IL-6, MAY HAVE A ROLE IN
 CC -1- SUBUNIT: HETEROOLIGOMER OF SIMILARITY.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: M92340; -; NOT_ANNOTATED_CS.
 CC PIR: A44257; A44257.
 CC HSSP: P40189; 1B0U.
 CC InterPro: IPR002995; CRIA.
 CC InterPro: IPR003526; RLITL.
 CC InterPro: IPR003529; Hematopo_receptor_L.F2.
 CC Pfam: PF00041; fn3; 3.
 CC SMART: SM00060; FN3; 3.
 CC PROSITE: PS01353; HEMATOPO_REC_L.F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Receptor: 3D structure Alternative splicing.
 CC STICK: 22
 CC CHAIN: 23 918
 CC FT DOMAIN 23 619 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC FT TRANSMEM 641 918 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 641 918 POTENTIAL.
 CC FT DOMAIN 124 322 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 124 322 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 325 423 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 424 517 FIBRONECTIN TYPE-III 3.
 CC FT DOMAIN 518 613 FIBRONECTIN TYPE-III 4.
 CC FT DOMAIN 725 755 FIBRONECTIN TYPE-III 5.
 CC FT DISULFED 28 54 SER-RICH.
 CC FT DISULFED 48 103
 CC FT DISULFED 134 144
 CC FT DISULFED 172 165
 CC FT DISULFED 457 463
 CC FT CARBOHYD 61 61
 CC FT CARBOHYD 61 61
 CC SEQUENCE 918 AA; 103522 MW; D013F3672D01D053 CRC64;
 CC -----
 CC Query Match 100.0%; Score 95; DB 1; Length 918;
 CC Best Local Similarity 100.0%; Seed No. 2,4e-07;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC 0Y 1 PUYKAKPNPNHLSYIN 17
 CC DB 216 PUYKAKPNPNHLSYIN 232
 CC RESULT 2

RC TISSUE-Placenta; PubMed=7579796;
RA MEDLINE=96078409; RA
RA MedGen=244444; RA
RA Akiyama M., F.R.A., Memura K., Kudo S., Fukuda M.:
RA "The European Bioinformatics Institute core 2 and localisation of the
RA beta-1,6-N-acetylglucosaminyltransferase gene family";
RA Glycobiology 5:417-425(1995).
RP [3]
RP TISSUE SPECIFICITY:
RA MEDLINE=98070745; PubMed=9403606;
RA Sasaki K., Kurita-Mura K., Ujima M., Angata K., Nakagawa S.,
RA Expression cloning of human N-
RA acetylglucosaminyltransferase that is essential for poly-N-
RA acetylactosamine synthesis." ;
RL Proc. Natl. Acad. Sci. U.S.A. 94:14294-14299(1997).
RT - POLY-N-BRANCHING ENZYME THAT CONVERTS LINAR INTO BRANCHED
CC POLY-N-ACETYLGLUCOSAMINOGLYCANS, INTRODUCES THE BLOOD GROUP I
CC ANTIGEN DURING EMBRYONIC DEVELOPMENT. THIS IS CLOSELY ASSOCIATED
CC WITH THE EXPRESSION OF ANOTHER BRANCHING ENZYME, TRANSFERRIN
CC CATALYTIC ACTIVITY. UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL
CC -1,4-N-ACETYL-D-GLUCOSAMINE-L-R = UDP + N-ACETYL-BETA-D-
CC GLUCOSAMINE-L-R + BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINE-L-R.
CC PATHWAY: GLYCOSYLATION.
CC - SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI.
CC TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PROSTATE AND
CC PANCREAS. IN THE EMBRYO, EXPRESSION IS LIMITED TO THE LIVER,
CC IN HUMAN BRAIN KIDNEY AND PANCREAS. NO EXPRESSION IN PLACENTA
CC OR LUNG. LIVER, SKELETAL MUSCLE, SPLEEN, THYMUS, TESTIS, OVARY AND
CC PERIPHERAL BLOOD LEUKOCYTES. IN PETTUS, HIGHLY EXPRESSED IN BRAIN
CC AND TO A LESSER EXTENT IN LUNG AND KIDNEY. BARRELY DETECTED IN
CC LIVER.
CC - DEVELOPMENTAL STAGE: ITS EXPRESSION INCREASES DRAMATICALLY DURING
CC DEVELOPMENT AND ONCOGENESIS.
CC - SIMILARITY: TO CORE 2 BRANCHING ENZYME (CGANT).

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CC or send an email to a licensee@isb-sib.ch).
DR EMBL: LA9659; AA81877.1; -
DR EMBL: Z19550; CA07610.1; -
DR EMBL: LA1607; AA959832.1; -
DR EMBL: LA1605; AA959832.1; JOINED.
DR EMBL: LA1606; AA959832.1; JOINED.
DR PIR: A6297; A6297.
DR MIR: G00429; -
DR MIR: S1008; -
DR InterPro: IP003406; Branch.
DR Pfam: PF02485; Branch: 1.
DR Transferrin: Glycosyltransferase: Transmembrane: Signal-anchor:
FM Golgi stack: Glycoprotein.
FM DOMAIN 1 6
FM TRANSMEM 7 25
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FM DOMAIN 36 400
FM CARBOHYD 37 37
FM CARBOHYD 255 255
FM CARBOHYD 314 314
FM CARBOHYD 388 388
SEQUENCE 400 AA: 45854 MW: 1459628590AUF43B CRC64:

Query Match: 49 5%; Score 47; DB 1; Length 400;
Best Local Similarity: 63 6%; Protein No 3;
Matches 7; Conservative 1; Idents 0; Gaps 0;

5 VKRPNNHLSV 15

-II IIIIII:-

Db	248	IKPPNNH.L1	258
RESULT	5		
DB131.HUMAN			
IC	BD11 MOUSE	STANDARD:	FT:
AD	PG7402:		400 AA.
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DE	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	N-ACETYLGALACTOSAMINE BETA 1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE		
DE	(EC 2.4.1.132) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (1-BRANCHING ENZYME)		
DE	(EC 2.4.1.132) (N-ACETYLGLUCOSAMINE BETA 1,6-N-ACETYLGALACTOSAMINYLTRANSFERASE).		
GN	GN2.		
GN	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
PN	NCBI_TaxID=10990.		
PN	SEQUENCE FROM N.A.		
RA	MEDLINE:91280061; PubMed:9134435;		
RA	Magnet A.D., Plukida M.;		
RT	Expression of the large I antigen forming beta1,6-N-		
RT	acetylglucosaminyltransferase in various tissues of adult mice. *		
RL	Glycobiology 7:285-293(1997).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC	ANTIGEN DURING EMBRYONIC AND DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINE:R = UDP + N-ACETYL-D-BETA-D-		
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.		
CC	-1- PATHWAY: GLYCOSYLATION. HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: HEP. I1 MEMBRANE PROTEIN. GOLGI.		
CC	-1- SUBCELLULAR LOCATION: BRANCHING ENZYME (GN2).		
CC	-1- FUNCTION: TRANSFERS N-ACETYL-1,6-N-ACETYLGLUCOSAMINE FROM AN		
CC			

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EMBL: X72576; CAS51168.1; -

DR PIR: S05383; S05383.

DR PIR: S06675; S06675.

DR InterPro: IPR001979; Apidacrin.

DR Pfam: PF00807; Apidacrin; 5.

DR Prodom: P123432; Apidacrin; 1.

DR TrEMBL: F00001979; Apidacrin.

KW Insect Immunity; Antibiotic; Hemolymph; Signal; Multigene family;

KW Cleavage on pair of basic residues; Repeat.

KW SIGNAL: 1 19 POTENTIAL.

FT PROPEP 1 19

FT PROPEP 35 42 APIDACRIN IB.

FT PROPEP 43 60

FT PROPEP 61 88 APIDACRIN IB.

FT PROPEP 71 98

FT PROPEP 91 98 APIDACRIN IB.

FT PROPEP 119 126

FT PROPEP 127 144

FT PEPTIDE 144 AA; 16539 MW; 66A1AD4CB7108D CRC64;

SQ SEQUENCE

Query Match 45.3%; Score 43; DB 1; Length 144;
Best Local Similarity 63.6%; Pred. No. 5,3;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PYKVKENPEP 11
11 : 111
47 PVIRPDEP 57

RESULT 10

AP14.APIME STANDARD; PRT: 168 AA.

ID AP14.APIME

AC 006601; P11525; P11526; P11527;

DT 01-OCT-1989 (rel. 12, Created)

DT 01-OCT-1989 (rel. 12, Last annotation update)

DT 01-JUN-1994 (rel. 29, Last annotation update)

DE APIDACRIN PRECURSOR, type 14.

GN APID14.

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Apidae; Apis.

OC NCBI-TaxID:1460;

OC RN 113-TaxID-1460;

RP SEQUENCE FROM N.A.

RX MEDLINE-93223697; PubMed-8467807;

RA Castels J., Josson K., Capaci T., Tempst P.;

RT "Apidacrin multipetide precursor structure: a putative mechanism for amplification of the insect antibacterial response.";

RT EMBD J. 12:1569-1578(1993).

RT 12

RS SEQUENCE OF APIDACRINS IN/IB/II.

RC TISSUE-Hemolymph;

RX MEDLINE-90005446; PubMed-2676519;

RA Castels P., Ampe C., Jacobs F., Vaecq M., Tempst P.;

RT "Apidacrin: antibacterial peptides from honeybees.";

RT EMBD J. 8:2387-2391(1989).

RT 1- FUNCTION: APIDACRINS HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY AGAINST NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL PROLIFERATION.

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CC EMBL: X72575; CAS51167.1; -

CC PIR: S05383; S05383.

DR PIR: S06675; S06675.

DR PIR: S06676; S06676.

DR PIR: S35330; S35330.

DR InterPro: IPR001979; Apidacrin.

DR Pfam: PF00807; Apidacrin; 5.

DR Prodom: P123432; Apidacrin; 1.

DR TrEMBL: F00001979; Apidacrin.

KW Insect Immunity; Antibiotic; Hemolymph; Signal; Multigene family;

KW Cleavage on pair of basic residues; Repeat.

KW SIGNAL: 1 19 POTENTIAL.

FT PROPEP 1 19

FT PROPEP 35 42 APIDACRIN II.

FT PROPEP 43 60

FT PROPEP 61 88 APIDACRIN II.

FT PROPEP 71 98

FT PROPEP 91 98 APIDACRIN IB.

FT PROPEP 119 124

FT PROPEP 125 142 APIDACRIN IB.

FT PROPEP 145 150

FT PEPTIDE 151 168

SQ SEQUENCE

Query Match 45.3%; Score 43; DB 1; Length 168;
Best Local Similarity 63.6%; Pred. No. 6,2;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PYKVKENPEP 11
11 : 111
103 PVIRPDEP 113

RESULT 11

AP73.APIME STANDARD; PRT: 283 AA.

ID AP73.APIME

AC 006602; P11525; P11526;

DT 01-OCT-1989 (rel. 12, Created)

DT 01-OCT-1989 (rel. 12, Last annotation update)

DT 01-JUN-1994 (rel. 29, Last annotation update)

DE APIDACRIN PRECURSOR, type 73 (FRAGMENT).

GN APID73.

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Apidae; Apis.

OC NCBI-TaxID:1460;

OC RN 113-TaxID-1460;

RP SEQUENCE FROM N.A.

RX MEDLINE-93223697; PubMed-8467807;

RA Castels J., Josson K., Capaci T., Tempst P.;

RT "Apidacrin multipetide precursor structure: a putative mechanism for amplification of the insect antibacterial response.";

RT EMBD J. 12:1569-1578(1993).

RT 12

RS SEQUENCE OF APIDACRINS IN/IB.

RC TISSUE-Hemolymph;

RX MEDLINE-90005446; PubMed-2676519;

RA Castels P., Ampe C., Jacobs F., Vaecq M., Tempst P.;

RT "Apidacrin: antibacterial peptides from honeybees.";

RT EMBD J. 8:2387-2391(1989).

RT 1- FUNCTION: APIDACRINS HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY AGAINST NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL PROLIFERATION.

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CC EMBL: X72577; CAS51169.1; -

CC PIR: S05383; S05383.


```

FT  TRANSMEM  122  142  POTENTIAL.
FT  TRANSMEM  152  174  POTENTIAL.
FT  TRANSMEM  186  206  POTENTIAL.
FT  TRANSMEM  207  227  CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM  706  726  POTENTIAL.
FT  TRANSMEM  730  750  POTENTIAL.
FT  TRANSMEM  770  791  POTENTIAL.
FT  DOMAIN    792  813  EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM  814  834  POTENTIAL.
FT  TRANSMEM  842  867  POTENTIAL.
FT  TRANSMEM  868  888  POTENTIAL.
FT  DOMAIN    889  924  CYTOPLASMIC (POTENTIAL).
FT  DOMAIN    913  929  CATALYTIC (POTENTIAL).
FT  DOMAIN    515  530  GLY-RICH.
FT  DOMAIN    569  602  GLY-RICH.
FT  DOMAIN    1278  1297  GLY/SER-RICH.
FT  DOMAIN    1277  1310  SER/GLY-RICH (ACIDIC).
FT  DOMAIN    1205  1240  GLY-RICH.
FT  CARBOHYD  800  807  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD  807  807  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  MUTAGEN   1026  1026  G->R: ABOLISHES CATALYTIC ACTIVITY.
SQ  SEQUENCE    2248 AA: 248899 MW:  E459C718BD018688 CRC64;

```

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Query Match      45 38:  Score 43; DB 1:  Length 2248;
Best Local Similarity 46.28; Pred. No. 99;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Oy  1  PYYKVKNPNNH.L 13
Db  1029  PERRKIDNPNSV 1041

```

Search completed: December 19, 2001, 16:26:20
 Job time: 575 sec

RESULT 2

09W609 PRELIMINARY: PRT: 918 AA.

AC 039559: 1 PYKVKPMPHNSV 11

DT 01-NOV-1999 (TEMBLrel. 12, Created)

DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE GLYCOPROTEIN 130 PRECURSOR.

GN Gp130.

OS Gallus gallus (chicken)

OC Archaeopteryx: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

NCBI_TaxID=9031;

FN [1]

SEQUENCE FROM N.A.

RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);

REMLINE-9902068; PubMed:80590; Rimbhorst U., Rohrer H.;

RT "The specification of sympathetic neurotransmitter phenotype depends

on gp130 cytokine receptor signaling.";

RL Development 125:4791-4801(1998).

RE EMBL: AJ011688; CnA2084.1; -

DR HSP: P40199; IAB01.

DR Interpro: IPR00396; CRIA.

DR Interpro: IPR00359; FcR1L1.

DR Interpro: IPR00359; Hematopo_receptor_L_F2.

DR Pfam: PF00041; fn3; 4.

DR SMART: SM00060; FN3; 3.

DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN.1.

DR Signal: 1

FT SIGNAL 1 26 POTENTIAL

FT SEQUENCE 918 AA: 102495 MW: 167625FP3E3613EF CRC64;

50

Query Match 53.74; Score 51; DB 13; Length 918;

Best Local Similarity 66.74; Pred. No. 10;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 221 PYKVKPMPHNSV 15

221 PYKVKPMPHNSV 235

RESULT 3

039599 PRELIMINARY: PRT: 225 AA.

AC 039559: 1 PYKVKPMPHNSV 11

DT 01-NOV-1998 (TEMBLrel. 01, Created)

DT 01-NOV-1998 (TEMBLrel. 01, Last sequence update)

DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)

DE EXTENSIN.

GN CYC15.

OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Ascerted; eusterids I; Gentianales; Apocynaceae; Catharanthus.

GN [1]; TaxID=4056;

SEQUENCE FROM N.A.

RX MEDLINE-98145469; PubMed-9484475;

RA Ito M., Kodama H., Komamine A., Watanabe A.;

"Expression of extensin genes is dependent on the stage of the cell

cycle and cell proliferation in suspension-cultured Catharanthus

roseus cells.";

REML: 986853; BAI31375.1; (1998).

DR EMBL: 986853; BAI31375.1; (1998).

DR Mendel: 24261; Catro2930; 24261.

SEQUENCE 225 AA: 25399 MW: 0253CDMAA7368D9 CRC64;

50

Query Match 49.54; Score 47; DB 10; Length 225;

Best Local Similarity 72.74; Pred. No. 10;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 91 PYKVKPMPHNSV 101

91 PYKVKPMPHNSV 101

RESULT 4

093404 PRELIMINARY: PRT: 346 AA.

AC 093404: 1 PYKVKPMPHNSV 11

DT 01-NOV-1998 (TEMBLrel. 08, Created)

DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE PROLACTIN RECEPTOR (FRAGMENT).

OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambicus).

OC Actinopterygii; Neopterygii; teleostei; Euteleostei; Euteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;

NCBI_TaxID=8127;

FN [1]

SEQUENCE FROM N.A.

RC TISSUE-CUL: Matsuda M., Mori T., Tetsuya H.;

RT "Expression of prolactin and cortisol receptor gene in early-life

stages of tilapia (Oreochromis mossambicus).";

RE Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF080247; AAC31825.1; -

DR HSP: P14787; IAB3.

DR Interpro: IPR00396; CRIA.

DR Interpro: IPR00359; FcR1L1.

DR Interpro: IPR00359; Hematopo_receptor_L_F1.

DR Pfam: PF00041; fn3; 2.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN.1.

DR NON_TER 346

FT SEQUENCE 346 AA: 39203 MW: E05AE4079326C530 CRC64;

50

Query Match 49.54; Score 47; DB 13; Length 346;

Best Local Similarity 64.34; Pred. No. 16;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 123 VYKVKPMPHNSV 136

123 VYKVKPMPHNSV 136

RESULT 5

082066 PRELIMINARY: PRT: 491 AA.

AC 082066: 1 PYKVKPMPHNSV 11

DT 01-NOV-1998 (TEMBLrel. 08, Created)

DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 14, Last annotation update)

DE PROLACTIN RECEPTOR.

GN Gp130.

OS Solanum tuberosum (potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Ascerted; eusterids I; Solanales; Solanaceae; Solanum.

GN [1]; TaxID=4113;

SEQUENCE FROM N.A.

RC STRAIN-CV DESIGNEE:

RA Menke U., Renault N., Mueller-Reeber B.;

Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

REML: AJ000997; CAA04449.1; -

DR EMBL: AJ000997; CAA04449.1; -

SEQUENCE 491 AA: 54112 MW: AAE5486860845F0C CRC64;

50

Query Match 49.54; Score 47; DB 10; Length 225;

```

Query Match          49.5%; Score 47; DB 10; Length 491;
Best Local Similarity 80.0%; Pred. No. 23;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 PYVKRKNP 10
      |||||
DB      259 PYVKRKRPP 268

RESULT      6
OYOUNA      PRELIMINARY; PRT: 1166 AA.
ID      OYOUNA
DT      01-MAY-2000 (TREMBLER, 13, Created)
DT      01-MAY-2000 (TREMBLER, 13, Last sequence update)
DT      01-JUN-2001 (TREMBLER, 17, Last annotation update)
DE      R NR-CAM 22 PROTEIN.
OS      Rattus sp.
OC      Eukaryota; Metazoa; Chordata; Scnrlata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]_TAXID-10116.
RP      SEQUENCE FROM N.A.
RA      MEDLINE-97103184; PubMed-8947556;
RX      Davis J.O., Lambert S., Bennett V.;
RT      Molecular composition of the node of Ranvier: identification of
RT      ankyrin-binding cell adhesion molecules neurofascin (mucin/third
RT      FNIII domain) and 35 kDa NCAM at node axon segments.
CC      -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DR      HSP; P20241; ICBP.
DR      InterPro: IPR003962; FNIII_repeat.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003598; IG_C2.
DR      InterPro: IPR003599; IG_C2.
DR      InterPro: IPR003598; IG_C2.
DR      InterPro: IPR003599; IG_C2.
DR      Pfam: PF00041; fn3; 4_IGMC.
DR      Pfam: PF00047; Ig; 6.
DR      PRINTS: PR00014; FNTPYRILL.
DR      SMART: SM00060; FN3; 4.
DR      SMART: SM00408; IGc2; 5.
DR      SMART: SM00410; IG_Like; 1.
DR      PROSITE: PS00250; IG_MHC; UNKNOWN.1.
KW      Repeat.
SQ      SEQUENCE      1166 AA; 128609 MW; 73662527DB07C8 CRC64;

Query Match          48.9%; Score 46.5; DB 11; Length 1166;
Best Local Similarity 52.3%; Pred. No. 64;
Matches      9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY      1 PYVKRKNP 10
      |||||
DB      594 PYDVP-PNPPDLN 609

RESULT      7
OYOUNA      PRELIMINARY; PRT: 1215 AA.
ID      OYOUNA
DT      01-JAN-1998 (TREMBLER, 05, Created)
DT      01-JAN-1998 (TREMBLER, 05, Last sequence update)
DT      01-JUN-2001 (TREMBLER, 17, Last annotation update)
DE      NC-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (FRAGMENT).
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Scnrlata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]_TAXID-10116.
RP      SEQUENCE FROM N.A.
RA      MEDLINE-97103184; PubMed-8947556;
RX      Davis J.O., Lambert S., Bennett V.;
RT      Molecular composition of the node of Ranvier: identification of
RT      ankyrin-binding cell adhesion molecules neurofascin (mucin/third
RT      FNIII domain) and NCAM at node axon segments.
CC      -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DR      HSP; P20241; ICBP.
DR      InterPro: IPR003962; FNIII_repeat.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003598; IG_C2.
DR      InterPro: IPR003599; IG_C2.
DR      InterPro: IPR003598; IG_C2.
DR      InterPro: IPR003599; IG_C2.
DR      Pfam: PF00041; fn3; 4_IGMC.
DR      Pfam: PF00047; Ig; 6.
DR      PRINTS: PR00014; FNTPYRILL.
DR      SMART: SM00060; FN3; 4.
DR      SMART: SM00408; IGc2; 5.
DR      SMART: SM00410; IG_Like; 1.
DR      PROSITE: PS00250; IG_MHC; UNKNOWN.1.
KW      Transmembrane; Signal; Cell adhesion; Repeat;
KW      Non-Ter.
SQ      SEQUENCE      1215 AA; 133966 MW; 6766508951B75CA CRC64;

```

Best Local Similarity: 52.9%; Pred. No. 67;
Matches: 9; Conservative: 3; Mismatches: 4; Indels: 1; Gaps: 1;

Oy 1 PYKXKPPPHNLSTYN 17
Db 643 PLYDV-PMPPELSTYN 658

RESULT 8
Q900Y5 PRELIMINARY: PRT: 279 AA.

DT 01-MAY-2000 (TRENBLREL.13, Created)
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update)
DT 01-JUN-2001 (TRENBLREL.17, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
NX NCBI_TaxID=9606;
RN 11

RP SEQUENCE FROM N.A.
RA Mada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: U08180; AAD05111.2; -;
DR HSSP: P40189; IBOU;
DR Interpro: IPR003548; CRIA;
DR Interpro: IPR003532; Hematopoietic_receptor_S_P2;
DR PROSITE: PS01356; HEMATOPOI_REC_S_F2; UNKNOWN_1.
KM Receptor.
SQ SEQUENCE 279 AA: 31658 MW: E7414F9F859EBB CRC64;

Query Match 48.4%; Score 46; DB 4; Length 279;
Best Local Similarity: 52.5%; Pred. No. 19;
Matches: 10; Conservative: 2; Mismatches: 2; Indels: 2; Gaps: 1;
Oy 4 KYKXNPPH-NLSTYN 17
Db 225 RVKDEPHNKNLSFIN 240

RESULT 9
Q29117 PRELIMINARY: PRT: 572 AA.

DT 029117, Q29033; Q29034; 01, Created
DT 01-NOV-1996 (TRENBLREL.01, Last sequence update)
DT 01-JUN-2001 (TRENBLREL.17, Last annotation update)
DE SUGARCOLE (PIG) (TRENBLREL.17, Last annotation update).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
NX NCBI_TaxID=9823;
RN 11

RP SEQUENCE FROM N.A.
RA MEDLINE-936527; PubMed-935902;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RL Characterization of a partial cDNA clone encoding porcine skeletal
muscle titin: comparison with rabbit and mouse skeletal muscle titin
sequences.
RT Comp. Biochem. Physiol. 105B:357-360(1993).
RN 12

RP SEQUENCE OF 67-121 AND 181-231 FROM N.A.

RA Tishbe R., Muroya S., Nakajima I., Chikuni K., Nakai H.;
RL "Skeletal muscle connectin primary structures as related to animal
species and muscle type."
RT J. Food Sci. 62:451-461(1997).
RN 1

-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.

DR EMBL: M97767; AA02940.1; -;
DR EMBL: D85840; BA01876.1; -;

DR EMBL: D85841; BA01897.1; -;
DR Interpro: IPR003962; FNIII_repeat.
DR Interpro: IPR003961; FN_III.
DR Interpro: IPR003598; Ig-C2.
DR Interpro: IPR003600; Ig-11k.
DR Interpro: IPR003006; Ig-MC.
DR Pfam: PF00041; fn3; 3.
DR Pfam: PF00041; Ig_2_PETIII.
DR Interpro: IPR000044; FN3_2.
DR SMART: SM00060; FN3_2.
DR SMART: SM00410; IG_1like; 1.
KM Repeat.
FT NON_TER 1 572
FT TER 572 572
SQ SEQUENCE 572 AA: 62977 MW: 742338093F9C9D CRC64;

Query Match 47.4%; Score 45; DB 6; Length 572;
Best Local Similarity: 52.9%; Pred. No. 54;
Matches: 9; Conservative: 3; Mismatches: 3; Indels: 2; Gaps: 1;

Oy 1 PYKXKPPPHNLSTYN 17
Db 49 PLYV-AKSPFNKXVD 63

RESULT 10
Q08001 PRELIMINARY: PRT: 693 AA.

DT 01-NOV-1996 (TRENBLREL.01, Created)
DT 01-NOV-1996 (TRENBLREL.01, Last sequence update)
DT 01-MAR-2001 (TRENBLREL.16, Last annotation update)
DE CHROMOSOME XII READING FRAME ORF YLR072W.
GN YLR072W.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NX NCBI_TaxID=4932;
RN 11

RP SEQUENCE FROM N.A.
RA POHL T.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN 12

RP MESS: Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z73441; CA697629.1; -;
DR SGP: S0004062; YLR072W.
SQ SEQUENCE 693 AA: 78212 MW: FACE2P16326B36F5 CRC64;

Query Match 47.4%; Score 45; DB 3; Length 693;
Best Local Similarity: 70.0%; Pred. No. 62;
Matches: 7; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;
Oy 1 PYKXKPPH 10
Db 371 PYKXKPPH 380

RESULT 11
Q10466 PRELIMINARY: PRT: 26926 AA.

DT 01-NOV-1996 (TRENBLREL.01, Created)
DT 01-NOV-1996 (TRENBLREL.01, Last sequence update)
DT 01-JUN-2001 (TRENBLREL.17, Last annotation update)
DE TITIN, HEART ISOFORM N2-B (EC 2.7.1.1-?) (CONNECTIN).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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OM protein - protein search, using SW model

Run on: December 19, 2001, 16:21:02 : Search time 78.52 seconds
(without alignments)
4.872 Million cell updates/sec

Title: US-09-202-104A-10

Accession: P1YKXKPNPNNLSWIN 17

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA*
1: /cgn2.6/pdata/2/1aa/5A.COMB.pep:*
2: /cgn2.6/pdata/2/1aa/5B.COMB.pep:*
3: /cgn2.6/pdata/2/1aa/6A.COMB.pep:*
4: /cgn2.6/pdata/2/1aa/6B.COMB.pep:*
5: /cgn2.6/pdata/2/1aa/PCUS.COMB.pep:*
6: /cgn2.6/pdata/2/1aa/Backlitest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	488	2	US-08-599-455B-5
2	95	100.0	488	4	US-08-599-455B-5
3	95	100.0	658	2	US-08-825-558-2
4	95	100.0	708	1	US-07-797-556-2
5	95	100.0	708	1	US-08-408-881-2
6	95	100.0	708	2	US-08-058-263-2
7	95	100.0	708	3	US-08-058-263-2
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9	95	100.0	708	3	US-08-058-263-2
10	95	100.0	708	3	US-08-058-263-2
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19	95	100.0	708	3	US-08-058-263-2
20	95	100.0	708	3	US-08-058-263-2
21	95	100.0	708	3	US-08-058-263-2
22	95	100.0	708	3	US-08-058-263-2
23	95	100.0	708	3	US-08-058-263-2
24	95	100.0	708	3	US-08-058-263-2
25	95	100.0	708	3	US-08-058-263-2
26	95	100.0	708	3	US-08-058-263-2
27	95	100.0	708	3	US-08-058-263-2
28	95	100.0	708	3	US-08-058-263-2
29	95	100.0	708	3	US-08-058-263-2
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34	95	100.0	708	3	US-08-058-263-2
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36	95	100.0	708	3	US-08-058-263-2
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42	95	100.0	708	3	US-08-058-263-2
43	95	100.0	708	3	US-08-058-263-2
44	95	100.0	708	3	US-08-058-263-2
45	95	100.0	708	3	US-08-058-263-2

28	42	44.2	185	2	US-08-445-073-9
29	42	44.2	185	2	US-08-585-258-9
30	42	44.2	185	2	US-08-585-258-9
31	42	44.2	185	2	US-08-585-258-9
32	42	44.2	185	2	US-08-585-258-9
33	42	44.2	185	2	US-08-585-258-9
34	42	44.2	185	2	US-08-585-258-9
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39	42	44.2	185	2	US-08-585-258-9
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41	42	44.2	185	2	US-08-585-258-9
42	42	44.2	185	2	US-08-585-258-9
43	42	44.2	185	2	US-08-585-258-9
44	42	44.2	185	2	US-08-585-258-9
45	42	44.2	185	2	US-08-585-258-9

ALIGNMENTS

RESULT 1
US-08-599-455B-5
Sequence 5, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Targila, Louis A.
INVENTOR: Targila, Robert J.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P. C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: SEQVIEW 1.0 Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/599,455B
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1997/0,142
PRIORITY APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 08-DEC-1995
ATTORNEY/NOTER INFORMATION:
NAME: Weiklich, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455b-5

Query Match 100.0%; Score 95; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 187 PYKVKPNPNHINLVIN 203

RESULT 2

US-09-069-781b-5
Sequence 5, Application US/09069781b
Patent No. 6287172
GENERAL INFORMATION:
APPLICANT: GEORGE A. LOUPE A.
APPLICANT: TEPPEL, ROBERT L.
APPLICANT: CALLEPER, JANICE A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER: IBM compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
CLASSIFICATION: 05/09/069, 781b
APPLICATION NUMBER: 05/09/069, 781b
FILING DATE: 29-APR-1996
PRIORITY NUMBER: 05/09/069, 781b
REFERENCE/DOCKET NUMBER: 05/08/654, 564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 05/08/708, 133
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 05/08/638, 524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 05/08/659, 455
FILING DATE: 22-APR-1996
APPLICATION NUMBER: 05/08/563, 153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 05/08/570, 142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 05/08/569, 485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 05/08/566, 622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 05/08/562, 663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: MELKLEJOHN, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07/34/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8900
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781b-5

Query Match 100.0%; Score 95; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 187 PYKVKPNPNHINLVIN 203

RESULT 3

US-08-825-558-4
Sequence 4, Application US/08825558
Patent No. 5963724
GENERAL INFORMATION:
APPLICANT: SMITH, STEPHEN K.
APPLICANT: BELLON, KIMBERLEY A.
TITLE OF INVENTION: Cp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 N. YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06/23, 0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-4

Query Match 100.0%; Score 95; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 216 PYKVKPNPNHINLVIN 232

RESULT 4

US-07797-556-2
Sequence 2, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: GEATING, DAVID P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 STATE: Seattle
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/308.881
 FILING DATE: 19911122
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathlyn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2607
 TELEPHONE: 206-587-0430
 TELEFAX: 206-587-0606
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-737-556-2

Query Match 100.0%; Score 95; DB 1; Length 708;
 Best Local Similarity 100.0%; Pred. No. 3,2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PYKKKPNPNLSVIN 17
 Db 216 PYKKKPNPNLSVIN 232

RESULT 5
 US-08-308-881-2
 Sequence 2, Application US/08/08881
 Patent No. 5783672
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308.881
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/249-553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathlyn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELERX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-308-881-2

Query Match 100.0%; Score 95; DB 1; Length 708;
 Best Local Similarity 100.0%; Pred. No. 3,2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PYKKKPNPNLSVIN 17
 Db 216 PYKKKPNPNLSVIN 232

RESULT 6
 US-09-058-263-2
 Sequence 2, Application US/09/058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/058.263
 FILING DATE: 09/09/058.263
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/308.881
 FILING DATE: 12-SEP-1994
 APPLICATION NUMBER: US 08/249-553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathlyn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-058-263-2

Query Match 100.0%; Score 95; DB 2; Length 708;
 Best Local Similarity 100.0%; Pred. No. 3,2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PYKVKPMPHNSYIN 17
| | | | | | | | | | | | | | | | | | | | | |
Db 216 PYKVKPMPHNSYIN 232

RESULT 7

US-09-059-099-2
Sequence 2, Application US/09059099
PCT-US95-06530-2
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: PC-TDS/MS-DOS, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 26-MAY-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 567-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%; Score 95; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PYKVKPMPHNSYIN 17
| | | | | | | | | | | | | | | | | | | | | |
Db 216 PYKVKPMPHNSYIN 232

RESULT 8

US-09-058-264-2
Sequence 2, Application US/09058264
PCT-US95-0610686
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-TDS/MS-DOS, Version 5.1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 26-MAY-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 26-MAY-1994

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: PC-TDS/MS-DOS, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,264
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 26-MAY-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 567-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-264-2

Query Match 100.0%; Score 95; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PYKVKPMPHNSYIN 17
| | | | | | | | | | | | | | | | | | | | | |
Db 216 PYKVKPMPHNSYIN 232

RESULT 9

PCT-US95-06530-2
Sequence 2, Application PCT/US9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-TDS/MS-DOS, Version 5.1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 26-MAY-1994
APPLICATION NUMBER: US/08/249,553
FILING DATE: 26-MAY-1994

```

1  ATTORNEY/AGENT INFORMATION:
2
3  NAME: Anderson, Kathryn A
4  REGISTRATION NUMBER: 33.1
5  REFERENCE/DOCKET NUMBER:
6  TELECOMMUNICATION INFORMATION:
7  TELEPHONE: (206) 587-0433
8  TELEFAX: (206) 233-0644
9  FAX:
10
11  INFORMATION FOR SEQ ID NO: 2
12
13  SEQUENCE CHARACTERISTICS:
14
15  LENGTH: 708 amino acids
16  TYPE: amino acid
17  TOPOLOGY: linear
18
19  MOLECULE TYPE: protein
20
21  PRT-0595-06530-2

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Query Match	100.0%	Score 55:	DB 5:	Length 708;
Best local similarity	100.0%	Pred. No. 3.2e-07;		
Matches 17:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Q7	1	PPYKKKRPPIHLSTVN	17	
Bb	216	PPYKKKRPPIHLSTVN	232	

```

1 RESULT 10
2 US-08-825-558-6
3 Sequence 6, Application US/08825558
4 Patent No. 5965724
5
6 GENERAL INFORMATION:
7 APPLICANT: SHAKRY, ANDREW
8 APPLICANT: SMITH, STEPHEN K.
9 APPLICANT: DEWITT, A.
10 TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
11 NUMBER OF SEQUENCES: 14
12 CORRESPONDENCE ADDRESS:
13 ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
14 STREET: 1100 NEW YORK AVENUE
15 CITY: WASHINGTON
16 STATE: DC
17 COUNTRY: USA
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: Patent Release #1.0, Version #1.30
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/825,558
25 FILING DATE: 15 MAR 1997
26 CLASS: 58
27 ATTORNEY/AGENT INFORMATION:
28 NAME: ESMOND, ROBERT W.
29 REGISTRATION NUMBER: 32,893
30 REFERENCE/DOCKET NUMBER: 0623_0330001
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (202)371-2600
33 TELEFAX: (202)371-2540
34 INFORMATION FOR SEQ ID NO: 6:
35 CHARACTERISTICS:
36 LENGTH: 918
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40
41 US-08-825-558-6

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Query Matchsimilarity	100.0%	Score 95:	DB 2:	Length 918:
Best Local Similarity	100.0%	Pred. No.	4.3e-07:	
Matches 17:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0
0Y	1	PYKAKKPPHMLSYIN	17	

Db 216 PYKVKPNP^HNL^SSVIN 232

RESULT 11
 US-08-118-906-14
 Sequence 14, Application US/08118906
 Patent No. 5484390CN
 GENETIC INFORMATION:
 APPLICANT: Blachuzen, Mattu
 APPLICANT: Blachuzen, Mattu F.A.
 TITLE OF INVENTION: Expression of the Developmental I
 TITLE OF INVENTION: Expression By a Cloned Human cDNA Encoding a Member of a
 TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase gene Family
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS: and Flores
 ADDRESS: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER REMARKS FORM:
 COMPUTER: IBM PC compatible disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release 4.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/118, 906
 FILING DATE: 09-SEP-1993
 CLASSIFICATION: C36
 AUTOMATIC REGISTRATION:
 NAME: Campbell Cathryn A.
 REGISTRATION NUMBER: 31 815
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-118-906-14

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Query Match 49.5%; Score 47; DB 1; Length 400;
Best local similarity 63.6%;
Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 VKENPNNLSV 15
      ||| |||||
Db 248 LKPPNNLTI 258

```

RESULT 12
 US-08-486-196-14
 ? Sequence 14, Application US/08486196
 ? Patent No. 5731420
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: FUKUDA, MINORU
 ?
 ? APPLICANT: Biernitzken, Matti F. A.
 ?
 ? INVENTOR: Biernitzken, Matti F. A.
 ?
 ? TITLE OF INVENTION: Expression of a
 ?
 ? TITLE OF INVENTION: Beta 1,5 N-Acetylglucosaminyltransferase Gene Family
 ?
 ? NUMBER OF SEQUENCES: 14
 ?
 ? CORRESPONDENCE ADDRESS:
 ?
 ? ADDRESSEE: Campbell and Flores
 ?
 ? STREET: 4370 La Jolla Village Drive, Suite 700
 ?
 ? CITY: San Diego
 ?
 ? STATE: California
 ?
 ? COUNTRY: USA

ZIP: 92122
 COMPUTER READABLE FORM:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9001
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-135-14

Query Match 49.5%; Score 47; DB 1; Length 400;
 Best Local Similarity 63.6%; Pred. No. 6.5;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 VRRPNNLSV 15
 DB 248 LKPPPHNLT 258

RESULT 13
 US-08-486-135-14
 Patent No. 5766910
 Application US/08486135
 GENERAL INFORMATION:
 APPLICANT: Fukuda, Minoru
 APPLICANT: Bierhuizen, Marti F.A.
 TITLE OF INVENTION: Expression of the Developmental I
 TITLE OF INVENTION: Antigen by a Cloned Human cDNA Encoding a Member of a
 NUMBER OF SEQUENCES: 14
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell, and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,135
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/118,906
 FILING DATE: 09-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9001
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9001
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-135-14

Query Match 49.5%; Score 47; DB 1; Length 400;
 Best Local Similarity 63.6%; Pred. No. 6.5;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 VRRPNNLSV 15
 DB 248 LKPPPHNLT 258

RESULT 14
 US-08-474-065-14
 Sequence 14, Application US/08474065
 Patent No. 5830465
 GENERAL INFORMATION:
 APPLICANT: Fukuda, Minoru
 APPLICANT: Bierhuizen, Marti F.A.
 TITLE OF INVENTION: Expression of the Developmental I
 TITLE OF INVENTION: Antigen by a Cloned Human cDNA Encoding a Member of a
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell, and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,065
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/118,906
 FILING DATE: 09-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9001
 TELECOMMUNICATION INFORMATION:

US-08-474-065-14

Query Match 49.5%; Score 47; DB 2; Length 400;
 Best Local Similarity 63.6%; Pred. No. 6.5;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 VRRPNNLSV 15
 DB 248 LKPPPHNLT 258

RESULT 15
NIS-09-233-

US-09-233-506-4

Sequence 4, Application US/09233506

Patent No. 6136580

GENERAL INFORMATION:

APPLICANT: Fukuda, Minoru

APPLICANT: Yeh, Jiunn-Chern

TITLE OF INVENTION: A Beta-1-6-N-Acetylglucosaminyltransferase That Forms

TITLE OF INVENTION: Core 2, Core 4 and I Branches

FILE REFERENCE: P-LJ 3415

CURRENT APPLICATION NUMBER: US/09/233,506

CURRENT FILING DATE: 1999-01-19

; NUMBER OF SEQ ID NOS: 14

NUMBER OF
SOFTWARE: Pa

; SEQ ID NO 4

; SEQ ID NO 4
; LENGTH: 400

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; LENGTH: 400
; TYPE: PRT
;

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TYPE: PRT
ORGANISM: Homo sapiens

Query Match 49.58; Score 47; DB 4; Length 400;

Best Local Similarity 63.68; Pred. No. 6.5;

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Matches      7;  Conservative      3;  Mismatches      1;  Indels      0;  Gaps      0;
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QY 5 VKPNRPHNL5V 15

QY 3 VKNPPHNLSV 13
: | | | | | :
: | | | | | :

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Db      248 LKRRPHNLTI 258

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UNRECORDED 238

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156:43 2001

US-09-202-104a-11.1rag

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:37; Search time 170.68 seconds
(Without alignments)
13,152 Million cell updates/sec

US-09-202-104a-11

Title: 146
Sequence: 1 EMGRPSTPILTKAVLWKEKFSAPED 28

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 522463 seqs, 74073390 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Genescq_1101.*

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2:	/SIDSB/gcgdata/genescq/genescqp/AA1982.DAT.*
3:	/SIDSB/gcgdata/genescq/genescqp/AA1983.DAT.*
4:	/SIDSB/gcgdata/genescq/genescqp/AA1984.DAT.*
5:	/SIDSB/gcgdata/genescq/genescqp/AA1985.DAT.*
6:	/SIDSB/gcgdata/genescq/genescqp/AA1986.DAT.*
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8:	/SIDSB/gcgdata/genescq/genescqp/AA1988.DAT.*
9:	/SIDSB/gcgdata/genescq/genescqp/AA1989.DAT.*
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12:	/SIDSB/gcgdata/genescq/genescqp/AA1992.DAT.*
13:	/SIDSB/gcgdata/genescq/genescqp/AA1993.DAT.*
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22:	/SIDSB/gcgdata/genescq/genescqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	28	19	AAW52211
2	146	100.0	182	27	AAW08805
3	146	100.0	315	21	AAW92200
4	146	100.0	323	10	AAW90527
5	146	100.0	325	21	AAW13389
6	146	100.0	325	21	AAW13390
7	146	100.0	344	20	AAW15071
8	146	100.0	344	20	AAW15072
9	146	100.0	360	20	AAW0804
10	146	100.0	360	21	AAW92199

12	146	100.0	419	20	AAW30938
13	146	100.0	468	10	AAW90525
14	146	100.0	468	10	AAW90284
15	146	100.0	468	14	AAW37215
16	146	100.0	468	17	AAW93164
17	146	100.0	468	17	AAW93165
18	146	100.0	477	21	AAW92197
19	146	100.0	500	18	AAW16547
20	146	100.0	515	21	AAW15104
21	146	100.0	525	18	AAW16546
22	146	100.0	543	20	AAW10789
23	146	100.0	552	20	AAW10789
24	146	100.0	552	20	AAW10789
25	146	100.0	690	21	AAW92185
26	146	100.0	1042	16	AAW01222
27	146	100.0	1158	21	AAW92404
28	146	100.0	1168	21	AAW92404
29	146	100.0	134	19	AAW0526
30	134	91.8	468	19	AAW0526
31	119	91.5	325	11	AAW06591
32	102	69.9	25	19	AAW52205
33	102	69.9	21	22	AAW85656
34	102	69.9	21	22	AAW85656
35	102	69.9	21	22	AAW85656
36	102	69.9	21	22	AAW85656
37	99	67.8	21	22	AAW85657
38	98	67.1	21	22	AAW85657
39	98	67.1	21	22	AAW85657
40	98	67.1	21	22	AAW85657
41	97	66.4	21	22	AAW88705
42	97	66.4	21	22	AAW88705
43	97	66.4	21	22	AAW88710
44	97	66.4	21	22	AAW88710
45	97	66.4	21	22	AAW88712

ALIGNMENTS

RESULT 1

ID	Seq2211	standard: peptide: 28 AA.
AC	AAW52211	
XX	09-JUN-1998 (first entry)	
XX	Interleukin-6 antagonist peptide.	
XX	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma; acquired immune deficiency syndrome-related lymphoma; immune response; rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy.	
XX	Alzheimer's disease.	
XX	Synthetic.	
OS	Homo sapiens.	
XX	W09748726-AL.	
XX	24-DEC-1997.	
XX	19-JUN-1997; 97MO-NL00345.	
XX	20-JUN-1996; 96EP-0201720.	
XX	(KOSTR) KOSTER H W.	
XX	Hochbe KHN. Van Leengood LMG;	
XX	WPI. 1998-063080/06.	
XX	New peptide(s) with interleukin-6 agonist or antagonist activity -	
PT	useful for treatment, prevention and diagnosis of IL-6 associated	

Human IL-6 receptor

B cell stimulatory

Sequence receptor

Interleukin-6 rece

Human IL-6 receptor

Human IL-6 receptor

Human IL-6 receptor

Human IL-6 receptor

Human IL-6 receptor

Human IL-6 receptor

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Human IL-6 receptor


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RESULT 6
XX AAB15389 standard; Protein: 325 AA.
AC AAB15389;
XX AAB15389;
DT 11-DEC-2000 (first entry)
XX Human Interleukin 6 receptor protein.
XX Human Interleukin-6 receptor; fungus: Pichia pastoris; PCR primer:
XX expression vector; immunoglobulin-like region; cytokine receptor region.
XX Homo sapiens.
XX Key Location/Qualifiers
XX MISC-difference 7/Note= "encoded by GGC"
XX MISC-difference 281 /Note= "encoded by CAA"
XX JP2000157280-A.
XX 13-JUN-2000.
XX 26-NOV-1998; 98JP-0335464.
XX 26-NOV-1998; 98JP-0335464.
XX (TOYO ) TOSOH CORP.
XX WPI: 2000-468203/41.
XX N-PSDB: AAB70701.
XX Yeasts transformed with IL-6 receptor gene -
XX Example 1: Page 6-8; 10pp; Japanese.
XX The invention relates to the production of human interleukin-6 receptor
XX protein in the fungus Pichia pastoris. The fungus has
XX been transformed with a recombinant expression vector encoding a gene
XX encoding an IL-6R protein having an immunoglobulin-like region and
XX cytokine receptor region and spanning amino acids from Leu20-Ala323. The
XX human IL-6R region was PCR amplified using the primers AAA70702-A70703.
XX This sequence represents the recombinant IL-6R protein of the invention.
XX Sequence 325 AA:
XX
XX Query Match 100.0%; Score 146; DB 21; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 1e-14;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EHGRRSTPSLTTRKAVLVKRFKQNSPAD 28
XX ||||||||||||||||||||||||
XX Db 114 ewgrrstpslttrkavlvkrfkqns pad 141
XX
XX RESULT 7
XX AAB15390 standard; Protein: 325 AA.
XX AAB15390;
XX AAB15390;
XX 15-DEC-2000 (first entry)
XX Bovine Interleukin-12 p35 subunit protein.
XX Antifungal; bovine; Interleukin 12; IL12; heterodimer; infection.
XX Bos taurus.
XX

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XX JP2000157274-A.
XX 13-JUN-2000.
XX 20-NOV-1998; 98JP-0331052.
XX 20-NOV-1998; 98JP-0331052.
XX (DNOC ) DATICHI PHARM CO LTD.
XX WPI: 2000-468201/41.
XX N-PSDB: AAB70708.
XX Preparation of bovine Interleukin 12 comprising using a vector
XX containing the gene encoding it; useful for the prevention and
XX treatment of chronic and opportunistic infections -
XX Example 1: Page 8; 11pp; Japanese.
XX The invention relates to a method for the preparation of bovine
XX Interleukin 12 (Boil12). Boil12 consists of a heterodimer of p35
XX and p40 subunits. Boil12 is produced by introducing into a host cell,
XX recombinant vectors containing genes encoding the p35 and p40 subunits.
XX This sequence represents the bovine IL12 p35 subunit. Interleukin 12
XX is used for the prevention and treatment of chronic infections and
XX opportunistic infections.
XX Sequence 325 AA:
XX
XX Query Match 100.0%; Score 146; DB 21; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 1e-14;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EHGRRSTPSLTTRKAVLVKRFKQNSPAD 28
XX ||||||||||||||||||||||||
XX Db 114 ewgrrstpslttrkavlvkrfkqns pad 141
XX
XX RESULT 8
XX AAB90528 standard; Protein: 344 AA.
XX AAB90528;
XX AAB90528;
XX 25-JAN-1990 (first entry)
XX B cell stimulating factor-2 receptor.
XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
XX Homo sapiens.
XX A08928720-A.
XX 27-JUL-1989.
XX 23-JAN-1989; 89AU-0028720.
XX 22-JAN-1988; 88JP-0012387.
XX 25-JAN-1988; 88JP-0012599.
XX 04-AUG-1988; 88JP-0194885.
XX 14-JAN-1989; 89JP-0007461.
XX (KISH ) TONAMITSU KISHIMOTO.
XX Kishimoto F.
XX WPI: 1989-264012/37.
XX N-PSDB: AAB90525.
XX Receptor protein for human B cell stimulating factor-2 - used for
XX developing prophylactic, therapeutic and diagnostic agents for

```


Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EHGCRSTSLTKKAVILYKRNQSPAD 28
|||||
Db 133 ewgprstsltkkavilvkkfqspad 160

RESULT 11

AA92199 standard; protein: 360 AA.

AA92199;

01-AUG-2000 (first entry)

Soluble human IL-6-R-alpha.

Soluble IL-6-R-alpha; cytokine; antagonist; CNF; receptor;

fusion protein; cytosolic; immunomodulator; osteopathic.

Homo sapiens.

MO20018332-A2.

06-APR-2000.

22-SEP-1999; 99MO-0622045.

25-SEP-1998; 98US-0101856.

19-MAY-1999; 99US-0313942.

(REGC-) REGENERON PHARM INC.

Stahl N, Yancopoulos GP;

WPI: 2000-293165/75.

Isolated nucleic acid molecule for treating cytokine-related diseases

or disorders encodes a fusion polypeptide capable of binding a cytokine

to form a nonfunctional complex

Example 4; Fig 15; 152pp; English.

The invention concerns production of antagonists to any cytokine that utilizes an alpha specifically determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the intermediate being specifically determined by the first beta signal transducing component of the extracellular domain of the first beta signal transducing component (8R-alpha-beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (cellary neurotrophic factor) family of cytokines. The invention provides the nucleic acid sequence of the functional antagonists, as they show that IL, in combination with the functional antagonists, can be used to block the action of the component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inactive. The heterodimers are used to treat the various native membrane-bound forms of their receptors. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.

Sequence 360 AA;

Query Match 100.0%; Score 146; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EHGCRSTSLTKKAVILYKRNQSPAD 28
|||||
Db 133 ewgprstsltkkavilvkkfqspad 160

RESULT 12

AA130938 standard; protein: 419 AA.

AA130938;

19-OCT-1999 (first entry)

Human IL-6 receptor/IL-6 fusion protein.

IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;

stem cell; platelet; reduced antigenicity.

Homo sapiens.

Synthetic.

Key

Protein

Location/Qualifiers

1-419

/note= "No start codon given"

JPI1196867-A.

27-JUL-1999.

09-JAN-1998; 98JP-0002921.

09-JAN-1998; 98JP-0002921.

(TOYU) TOSOH CORP.

WPI: 1999-196648/42.

N-PSDB; AA209202.

New interleukin-6 receptor-interleukin-6 fused protein and gene

used for growth of bone marrow stem cells and platelets

Example 1; Page 5-8; 8pp; Japanese.

This invention describes a novel gene which encodes a fusion protein of interleukin-6 (IL-6) receptor and bone marrow stem cell antigen. The fusion protein has applications for the growth of bone marrow stem cells and platelets. Transmission of a signal of IL-6 to target cells for stimulation with reduced antigenicity is possible. This sequence represents the IL-6 receptor/IL-6 fusion protein described in the invention.

Sequence 419 AA;

Query Match 100.0%; Score 146; DB 20; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EHGCRSTSLTKKAVILYKRNQSPAD 28

Db 18 ewgprstsltkkavilvkkfqspad 45

RESULT 13

AA90525 standard; protein: 468 AA.

AA90525;

```

XX 23-JAN-1990 (first entry)
XX B cell stimulating factor-2 receptor.
XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
XX Homo sapiens.
XX A08928720-A.
XX 27-JUL-1989.
XX 23-JAN-1989; 89AU-0028720.
XX 22-JAN-1988; 88JP-0012387.
XX 25-JAN-1988; 88JP-0012599.
XX 04-AUG-1988; 88JP-0194885.
XX 14-JAN-1989; 89JP-0007461.
XX (KISH ) TMDMITSU KISHIMOTO.
XX Kishimoto T.
XX WPI: 1989-264012/37.
XX N-PSDB: AAP90525.
XX Receptor protein for human B cell stimulating factor-2; used for
XX developing prophylactic, therapeutic and diagnostic agents for
XX associated disorders.
XX Claim 2; page 36; 76pp; english.
XX The BSP2 receptor is derived from a monocytic U937 cell line. It can be
XX used to develop diagnostic and therapeutic pharmaceuticals, as agents to
XX relate disease and disease susceptibility. It is to be
XX used to study an immune mechanism with which BSP-2 or the receptor is
XX concerned.
XX Sequence 468 AA;
XX
XX Query Match 100.0%; Score 146; DB 10; Length 468;
XX Best Local Similarity 100.0%; Pred. No. 1,5e-14;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EMGPRSTPLTTKAVILVRFQNSPAED 28
XX ||||||||||||||||||||||||
XX DB 133 ewgprstplttkavilvrfqnspead 160
XX
XX RESULT 14
XX AAP90284
XX ID AAP90284 standard; Protein: 468 AA.
XX
XX AAF90284;
XX
XX 31-MAR-1992 (first entry)
XX Sequence of a receptor protein for human B cell stimulating
XX factor-2 (BSP2 receptor).
XX B cell; Immune disorder; therapy; diagnosis; prophylaxis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX PH 2..22 /label= hydrophobic region
XX PT 362..386 /label= hydrophobic region
XX Region
XX EP325474-A.

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XX PD 26-JUL-1989.
XX 20-JAN-1989; 89EP-0300536.
XX 14-JAN-1989; 89JP-0017461.
XX 22-JAN-1988; 88JP-0012387.
XX 25-JAN-1988; 88JP-0012599.
XX 04-AUG-1988; 88JP-0194885.
XX 20-JAN-1989; 89JP-0009774.
XX (KISH ) KISHIMOTO T.
XX Kishimoto T.
XX WPI: 1989-214667/30.
XX N-PSDB: AAN90340.
XX Receptor protein for human B cell stimulating factor-2 - optd. by
XX recombinant DNA techniques and used as diagnostic, prophylactic or
XX therapeutic agent.
XX Claim 2; page 19-21; 63pp; English.
XX The cDNA in AAN90340 was derived from monocytic cell line U937.
XX Isolated BSP2 receptor and DNA encoding it are claimed, as are
XX (b) expression vectors; (c) host organisms; (d) antibodies; and
XX (e) hybridomas.
XX Sequence 468 AA;
XX
XX Query Match 100.0%; Score 146; DB 10; Length 468;
XX Best Local Similarity 100.0%; Pred. No. 1,5e-14;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EMGPRSTPLTTKAVILVRFQNSPAED 28
XX ||||||||||||||||||||||||
XX DB 133 ewgprstplttkavilvrfqnspead 160
XX
XX RESULT 15
XX AAR37215
XX ID AAR37215 standard; Protein: 468 AA.
XX
XX AAR37215;
XX
XX 13-SEP-1993 (first entry)
XX
XX IL-6 receptor.
XX Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
XX interleukin-6; interleukin-6 myeloma; binding; solubility; signal transfer;
XX disease; intracellular.
XX Synthetic.
XX OS JP0501892-A.
XX 16-APR-1993.
XX 02-OCT-1991; 91JP-0255521.
XX 02-OCT-1991; 91JP-0255521.
XX (CHUS ) CHUGAI PHARM CO LTD.
XX (KISH ) KISHIMOTO T.
XX (TOSH ) TOSH CO.
XX WPI: 1993-161739/20.
XX N-PSDB: AAO41746.
XX New Interleukin-6 receptor deriv. - for treating diseases caused

```

PT by IL-6, e.g. multiple myeloma
XX
XS Disclosure; Page 10-12; 23pp; Japanese.
XX
XX This sequence represents an interleukin-6 (IL-6) receptor. Variants
CC of the receptor lacking either the immunoglobulin-like domain or the
CC transmembrane and intracellular domain have IL-6 binding ability and
CC signal transfer ability. Either the full length or truncated IL-6
CC receptors may be used for diseases caused by IL-6 such as multiple
XX myeloma.
XX
SQ Sequence 468 AA:

Query Match 100.0%; Score 146; DB 14; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EWGPRSTGSLTAVLVKXKONSRAED 28
|||||
Db 133 ewgprstgsltkavllvrxkqspaed 160

Search completed: December 19, 2001, 16:19:37
Job time: 362 sec

PT diseases
 PA Claim 6; Page 17; 28pp; English.
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome, AIDS, osteoporosis, Alzheimer's disease etc.) also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC be immunogenic and therefore they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies, the mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC Sequence 21 AA:
 SQ
 Query Match 100.0%; Score 102; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.3e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PRSPSTLTTRKAVLYVRKNS 21
 1 prspstlttrkavlvrkns 21
 Db 1 prspstlttrkavlvrkns 21
 RESULT 2
 AAB8666 standard; Peptide: 21 AA.
 XX AAB8666:
 AC AAB8666:
 DT 23-MAY-2001 (first entry)
 DE Human interleukin-6 domain II fragment #1.
 XX Interleukin-6, ligand, IL-6 receptor; antagonist; cancer; allergy;
 XX rheumatoid arthritis; diabetes; multiple sclerosis; infection;
 XX autoimmune disease; inflammatory disease.
 OS Homo sapiens.
 FN WO200116166-A2.
 PA 08-MAR-2001.
 PE 25-AUG-2000; 2000MO-US23490.
 PR 27-AUG-1999; 99US-0151277.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Saxinger C;
 XX WPI: 2001-244395/25.
 PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand
 PT with the IL-6 receptor, and the nucleic acids that encode them, useful
 PT for treating e.g. inflammation and autoimmune diseases -
 XX Example 2; Page 44; 98pp; English.

CC The present invention describes a number of peptides which are able to
 CC bind to the human interleukin-6 (IL-6) receptor and inhibit IL-6 binding.
 CC These peptides are useful in the treatment of diseases associated with abnormal
 CC IL-6 expression, including multiple myeloma, plasmacytoma, hematological
 CC diseases such as plasma cell dyscrasias, leukemia and lymphoma,
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.
 CC Sequence 21 AA:
 SQ
 Query Match 100.0%; Score 102; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.3e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PRSPSTLTTRKAVLYVRKNS 21
 1 prspstlttrkavlvrkns 21
 Db 1 prspstlttrkavlvrkns 21
 RESULT 3
 AAB8662 standard; Peptide: 21 AA.
 XX AAB8662:
 AC AAB8662:
 DT 23-MAY-2001 (first entry)
 DE Human interleukin-6 domain II fragment #17.
 XX Interleukin-6, ligand, IL-6 receptor; antagonist; cancer; allergy;
 XX rheumatoid arthritis; diabetes; multiple sclerosis; infection;
 XX autoimmune disease; inflammatory disease.
 OS Homo sapiens.
 FN WO200116166-A2.
 PA 08-MAR-2001.
 PE 25-AUG-2000; 2000MO-US23490.
 PR 27-AUG-1999; 99US-0151277.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Saxinger C;
 XX WPI: 2001-244395/25.
 PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand
 PT with the IL-6 receptor, and the nucleic acids that encode them, useful
 PT for treating e.g. inflammation and autoimmune diseases -
 XX Example 2; Page 44; 98pp; English.
 CC The present invention describes a number of peptides which are able to
 CC bind to the human interleukin-6 (IL-6) receptor and inhibit IL-6 binding.
 CC These are useful in the treatment of diseases associated with abnormal
 CC IL-6 expression, including multiple myeloma, plasmacytoma, hematological
 CC diseases such as plasma cell dyscrasias, leukemia and lymphoma,
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.
 CC Sequence 21 AA:
 SQ
 Query Match 100.0%; Score 102; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.3e-11;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 PRSTPSLTTRKAVLVYRKFRNS 21
 DB 1 PRSTPSLTTRKAVLVYRKFRNS 21

RESULT 4
 AAB8698 standard: peptide; 21 AA.
 AAB8698:
 23-MAY-2001 (first entry)
 Human Interleukin-6 domain II fragment #33.
 Interleukin-6; ligand; IL-6 receptor; antagonist; cancer; allergy;
 rheumatoid arthritis; diabetes; multiple sclerosis; infection;
 autoimmune disease; inflammatory disease.
 Homo sapiens.
 MO20011616-A2.
 08-MAR-2001.
 25-AUG-2000: 2000MO-US23490.
 27-AUG-1999: 99US-0151277.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Saxinger C;
 WPI: 2001-244395/25.
 polypeptides which inhibit the binding of interleukin (IL)-6 ligand
 with the IL-6 receptor, and the nucleic acids that encode them, useful
 for treating e.g. inflammation and autoimmune diseases -

Example 2: Page 45; 98pp; English.

The present invention describes a number of peptides which are able to
 block the binding of interleukin-6 (IL-6) to its receptor. These
 peptides are useful in the treatment of diseases associated with abnormal
 IL-6 expression, including multiple myeloma, plasmacytoma, hematological
 diseases such as plasma cell dyscrasias, leukemia and lymphoma,
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.

Sequence 21 AA:

Query Match 100.0%; Score 102; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9, 3e-11;
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 PRSTPSLTTRKAVLVYRKFRNS 21
 DB 1 PRSTPSLTTRKAVLVYRKFRNS 21

RESULT 5
 AAM52211 standard: peptide; 28 AA.
 AAM52211:
 AAM52211:
 09-JUN-1998 (first entry)

DE Interleukin-6 antagonist peptide.
 KW Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
 KW acquired immune deficiency syndrome-related lymphoma; immune response;
 KW rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
 KW Alzheimer's disease.
 OS Synthetic.
 OS Homo sapiens.
 PN MO9748728-A1.
 PD 24-DEC-1997.
 PD 19-JUN-1997: 97MO-NL00345.
 PR 20-JUN-1996: 96EP-0201720.
 PA (KOSTY) KOSTER H N.
 PI Hoebe KHN, van Leengoed LMG;
 DI WPI: 1998-063080/06.
 PT New peptide(s) with interleukin-6 agonist or antagonist activity -
 PT useful for treatment, prevention and diagnosis of IL-6 associated
 PT diseases

Claim 7: Page 17; 28pp; English.

This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC or many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, postmenopausal
 CC osteoporosis, chronic hepatitis, diabetes, multiple sclerosis, IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC hepatotoxic). In contrast no human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.

Sequence 28 AA:

Query Match 100.0%; Score 102; DB 19; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1, 3e-10;
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 PRSTPSLTTRKAVLVYRKFRNS 21
 DB 4 PRSTPSLTTRKAVLVYRKFRNS 24

RESULT 6
 AAM00403 standard: peptide; 182 AA.
 AAM00403:
 AAM00403:
 29-AUG-1996 (first entry)
 Interleukin-6 antagonist peptide.

KW	IL-6; antagonist; autoimmune disease.
OS	Synthetic.
PM	JF07324097-A.
XX	
PD	12-DEC-1995.
XX	
PF	30-MAY-1994; 94JP-0117259.
XX	
XX	30-MAY-1994; 94JP-0117259.
XX	
PA	(DAIIC) DAIGEL CHEM IND LTD.
XX	(FUJII) FUJISAMA PHARM CO LTD.
DR	WPI; 1996-065476/07.
PT	Interleukin 6 antagonist - useful for treating autoimmune diseases
PM	
XX	Claim 1, Page 2; 19pp; Japanese.
CC	New IL-6 antagonists are provided which are of formula X-W-Y, in
CC	which X is H or an amino-protecting group, Y is OH or a carboxy-
CC	protecting group, and W is a peptide containing all or part of the
CC	sequence as given in AA00401, AA00402, AA00403 (the present sequence)
CC	or AA00404, where any free mercapto groups in the sequence are
CC	protected by a protecting group.
CC	The present sequence (AA00428 - AA00435) are claimed as new chemical
CC	compounds. The IL-6 antagonists are useful for treating autoimmune
CC	diseases.
XX	
XX	Sequence 182 AA:
QY	Query Match 100.0%; Score 102; DB 17; Length 182;
	Best Local Similarity 100.0%; Pred NO 1, 2e-09;
DB	Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY	1 PRSTSLTAAVLKRRKNS 21 17 prspsltkavllvkrkqs 37
RESULT 7	
ID	AA070805
XX	AA070805 standard; protein: 315 AA.
AC	
XX	AA070805;
PT	03-FEB-1999 (first entry)
DE	Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
KW	gp130; cytokine antagonist; interleukin; gamma-Interferon;
KW	granulocyte macrophage colony-stimulating factor; J peptide;
KW	transforming growth factor-beta.
XX	
XX	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Protein 1..313
PR	/note= "Truncated Interleukin (IL)-6R-alpha domain"
PN	US5444099-A.
PM	
XX	01-DEC-1998.
XX	
PF	27-NOV-1995; 95US-0563105.
XX	
XX	27-NOV-1995; 95US-0563105.
XX	
PR	20-OCT-1993; 93US-0140222.
XX	
XX	(REGC-) REGENERON PHARM INC.

P1	Economides A,	Stahl N,	Tanopoulos GD;
X1			
D1	WPI, 1999-044669/OK.		
X1			
P7	Cytokine antagonists - comprising extracellular domains of		
PT	specificity-determining and signal-transducing components of		
X7	cystokine receptor		
PS			
XS	Example 4; Fig 16; 46pp; English.		
CC	The present sequence represents the amino acid sequence of interleukin		
CC	(IL)-R-alpha-113 domain. The protein is used in the course of the		
CC	Invention. The specification describes cytokine antagonists comprising		
CC	only the extracellular domain of the specificity-determining component of		
CC	the cytokine receptor and the extracellular domain of a cytokine		
CC	signal-transducing component of the cytokine receptor. The		
CC	antagonist also comprises at least one additional amino acid residue		
CC	gamma-interferon or transforming growth factor-beta (TGF-beta). The		
CC	antagonist is capable of binding the cytokine to form a nonfunctional		
CC	complex. The compounds have therapeutic activity as cytokine antagonists		
CC	and can also be used in assays for identifying novel agonists and		
CC	antagonists of cytokines.		
XQ			
X1	Sequence 315 AA:		
X1			
Query Match	100.0%; Score 102;	DB 20;	Length 315;
Best Local Similarity	100.0%;	Pred. No. 2, 2e-09;	
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
OY	1 PESTSLTLTKAVLLVKKFNS 21		
Db	136 PESTSLTKAVLLVKKFGNS 156		
RESULT 8			
AAY92200			
ID	AAY92200 standard; protein, 315 AA.		
X1			
X1	AAY92200:		
DT	01-AUG-2000 (first entry)		
XX			
DE	Soluble human IL-6-R-alpha-313.		
KM	Soluble IL-6-R-alpha-313; cytokine; antagonist; CMTF; receptor;		
KX	fusion protein; cytototoxic; immunomodulator; osteopetritic.		
OS	Homo sapiens.		
FH			
FT	Key Location/Qualifiers		
ET	Protein I..313		
FT	/label= truncated_IL-6-R-alpha		
FT	peptide 313..326		
FT	/note= "Thr-Gly bridge"		
XX			
PN	MO200018937-AZ.		
PD			
PD	06-APR-2000.		
XX			
PF	22-SEP-1998; 99MC-US22045.		
PR	25-SEP-1998; 98US-0101858.		
PA	19-MAY-1999; 99US-0313942.		
XX			
PA	(RECE-) REGENERON PHARM INC.		
XT	Stahl N, Tanopoulos GD;		
DN	WPI, 2000-29315/25.		
XX			

PT Isolated nucleic acid molecule for treating cytokine-related diseases
 CC or disorders encodes a fusion polypeptide capable of binding a cytokine
 CC to form a nonfunctional complex
 CC

Example 4: Fig 16: 152pp: English.

The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (ter alpha) and the extracellular domain of the first beta signal transducing component of the second beta signal transducing component form heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, the first beta signal transducing component, and the second beta signal transducing component, can be formed, it will be effective in blocking the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of p140. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides of the invention are useful for the treatment of disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.

Sequence 315 AA:

Query Match 100.0%; Score 102; DB 31; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 prpstsltkkavllvkrkfgs 156

1 PRGSTSLTKKAVLLVKKRFGS 21

|||||

RESULT 9
 AAP90527 standard; protein: 323 AA.

AAP90527;

25-JAN-1990 (first entry)

B cell stimulating factor-2 receptor.

B cell stimulating factor-2 receptor; monocyte U937 cell line.

Hom sapiens.

AA0828720-A.

27-JUL-1989.

23-JAN-1989; 89AU-0028720.

22-JAN-1988; 88JP-0012387.

25-JAN-1988; 88JP-0012599.

14-AUG-1988; 88CP-0194885.

14-JAN-1989; 89CP-0007401.

(KISH) TADAMITSU KISHIMOTO.

Kishimoto T;

DR WPI: 1989-264012/37.

DR N-PSDB; AAP90525.

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Receptor protein for human B cell stimulating factor-2 - used for developing prophylactic, therapeutic and diagnostic agents for associated disorders.

Claim 6; page 39; 76pp: english.

The BSEF receptor has amino acids at the C-terminal deleted. The receptor is derived from a monocyte U937 cell line. It can be used to develop prophylactic and therapeutic pharmaceuticals, as agents to relate diseases and disorders to abnormal BSEF prodn. It can also be used to study an immune mechanism with which BSEF 2 or the receptor is concerned.

Sequence 323 AA:

Query Match 100.0%; Score 102; DB 10; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 prpstsltkkavllvkrkfgs 156

1 PRGSTSLTKKAVLLVKKRFGS 21

|||||

RESULT 10
 AAP90527 standard; protein: 325 AA.

AAB15389;

11-DEC-2000 (first entry)

Human interleukin 6 receptor protein.

Human interleukin-6 receptor; fungus; Pichia pastoris; PCR primer; expression vector; Immunoglobulin-like region; cytokine receptor region.

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The invention relates to the production of human interleukin-6 receptor (IL-6) protein in the fungus Pichia pastoris. The fungus was transformed with an expression vector (pOUC3-A20L) containing a gene encoding human interleukin-6 receptor protein. The recombinant and cytokine receptor region and spanning amino acids from Leu30-A1a323. The human IL-6R region was PCR amplified using the primers AAAT0702-A70703. This sequence represents the recombinant IL-6R protein of the invention.

SQ Sequence 325 AA:
 Query Match 100.0%; Score 102; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 2,3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRSPSLTTRKAVLVLRKFGNS 21
 117 PRSPSLTTRKAVLVLRKFGNS 137
 DB 117 PRSPSLTTRKAVLVLRKFGNS 137
 RESULT 11
 AAB15390
 ID AAB15390 standard; protein: 325 AA.
 AC AAB15390:
 DT 15-DEC-2000 (first entry)
 DE Bovine Interleukin-12 p35 subunit protein.
 DX Anti-infective; bovine; interleukin 12; IL12; heterodimer; infection.
 KM Bos taurus.
 OS JP2000157274-N.
 PN 13-JUN-2000.
 PD 20-NOV-1998; 98JP-0331052.
 PE 20-NOV-1998; 98JP-0331052.
 PF (DANC) DATICHI PHARM CO LTD.
 PA WPI: 2000-468201/41.
 DR N-PSDB: AAA70708.
 DX Preparation of bovine interleukin 12 comprising using a vector
 PT treatment of chronic and opportunistic infections.
 PS Example 1: Page 8; 11pp; Japanese.
 XX The invention relates to a method for the preparation of bovine
 CC interleukin 12 (bIL12). bIL12 consists of a heterodimer of p35
 CC and p40 subunits. The p35 subunit is encoded by the p35 gene.
 CC Recombinant vectors containing genes encoding the p35 and p40 subunits.
 CC This sequence represents the bovine IL12 p35 subunit. Interleukin 12
 CC is used for the prevention and treatment of chronic infections and
 CC opportunistic infections.
 CC XX
 SQ Sequence 325 AA:
 Query Match 100.0%; Score 102; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 2,3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRSPSLTTRKAVLVLRKFGNS 21
 117 PRSPSLTTRKAVLVLRKFGNS 137
 DB 117 PRSPSLTTRKAVLVLRKFGNS 137
 RESULT 12
 AAP90528
 ID AAP90528 standard; protein: 344 AA.
 AC AAP90528:
 DT 25-JAN-1990 (first entry)
 XX

DE B cell stimulating factor-2 receptor.
 XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
 KM Homo sapiens.
 OS A08928720-A.
 PN 27-JUL-1989.
 PD 23-JAN-1989; 89AU-0028720.
 PE 22-JAN-1988; 88JP-0012387.
 PR 25-JAN-1988; 88JP-0012599.
 PR 04-AUG-1988; 88JP-0194885.
 PR 14-JAN-1989; 89JP-0007461.
 PA (KISH)-7ADAMITSU KISHIMOTO.
 DX Kishimoto T;
 DR WPI: 1989-264012/37.
 DR N-PSDB: AAP90525.
 KM Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 CC associated disorders.
 PS Claim 7; page 40; 76pp; English.
 XX The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a cDNA library and used to develop
 CC diagnostic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
 CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 CC XX
 SQ Sequence 344 AA:
 Query Match 100.0%; Score 102; DB 10; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2,4e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRSPSLTTRKAVLVLRKFGNS 21
 136 PRSPSLTTRKAVLVLRKFGNS 156
 DB 136 PRSPSLTTRKAVLVLRKFGNS 156
 RESULT 13
 AAY55071
 ID AAY55071 standard; protein: 345 AA.
 AC AAY55071:
 DT 25-FEB-2000 (first entry)
 DE SR345 protein sequence.
 DX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KM antigen-binding cell; secreted functional protein; antigenic protein;
 KM protein isolation; diagnosis; SR345 protein.
 CC Homo sapiens.
 CC MO9960113-A1.
 PD 25-NOV-1999.
 PE 30-APR-1999; 99MO-JP02341.
 PR 20-MAY-1998; 98JP-0138652.
 PR 01-OCT-1998; 98JP-0273876.
 XX

PA	(CHUS) CHUGAI SEIYAKU KK.
PI	Tsuchiya M., Salto M., Ontomo T.
PK	
PL	NPJ: 2000-03982/03.
PM	
PN	N-PSDB: AA240288.
PP	
PT	Efficient and selective isolation of a gene encoding membrane protein
PU	with low or no antigenic binding activity, for diagnosis, study of, and
PV	production of drugs treating abnormal functions of the protein
PX	
QA	
QB	
QC	Example 1; Page 49-52; 120pp; Japanese.
QD	
QE	This sequence represents the SR45 protein.
QF	The invention relates to a method for isolating a gene encoding a
QG	membrane-bound protein, comprising introducing a vector into a cell,
QH	contracting an antigen with the cell expressing the fused protein encoded
QI	by the vector on its surface to select an antigen-binding cell, and
QJ	isolating the cDNA. The vector contains DNA encoding a selectable
QK	marker protein, an origin of replication, and binding affinity, and a cDNA
QL	insertion site for a probe downstream of the marker gene.
QM	This method can be used to isolate a membrane-bound protein for diagnosis and
QN	study. It can also be used for producing drugs treating abnormal
QO	functions of the protein. Such a technique is efficient and selective,
QP	which is different from the prior-art transmembrane trap (TMT) method
QQ	wherein an epitope recognised by an antibody is carried in a fused
QR	
QS	Sequence 345 AA.
QT	
QU	
QV	Query Match 100.0%; Score 102; DB 21; Length 345;
QW	Best Local Similarity 100.0%; Pred. No. 2,4e-09;
QX	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	1 PRSTGSEITKAVILYKTKNS 21
QZ	
RA	136 PRSTGSEITKAVILYKTKNS 156
RB	
RC	
RD	
RE	RESULT 14
RF	AAW07004
RG	AAW07004 standard; protein: 360 AA.
RH	
RI	AAW07004:
RJ	
RK	03-FEB-1999 (first entry)
RL	
RM	
RN	Amino acid sequence of the interleukin (IL)-6R-alpha domain.
RO	
RP	gp130; cytokine antagonist; Interleukin; gamma-Interferon;
RQ	granulocyte macrophage colony-stimulating factor; J peptide;
RS	transforming growth factor-beta.
RT	
RU	Synthetic.
RV	
RW	
RX	Key
RY	Location/Qualifiers
RZ	Protein 1..358
SA	US5644099-A
SB	/note="soluble interleukin (IL)-6R-alpha domain"
SC	
SD	01-DEC-1998.
SE	
SF	27-NOV-1995; 9505-0563105.
SG	
SH	27-NOV-1995; 9505-0563105.
SI	20-OCT-1995; 9505-0140222.
SJ	
SK	(RECE-) REGENERON PHARM INC.
SL	
SM	Economides A., Stahl N., Yancopoulos CD;
SN	
SO	
SP	
SQ	
SR	
SS	
ST	
SU	
SV	
SW	
SX	
SY	
SZ	
TA	
TB	
TC	
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XH	
XI	
XJ	
XK	
XL	
XM	
XN	
XO	
XP	
XQ	
XR	
XS	
XT	
XU	
XV	
XW	
XX	
XY	
XZ	
YA	
YB	
YC	
YD	
YE	
YF	
YG	

DR WP1; 1999-044669/01.
xx
xx Cytokine antagonists - comprising extracellular domains of
PT specifically-determining and signal-transducing components of
PT cytokine receptor
xx
PS Example 4; Fig 15; 46pp; English.

CC The present sequence represents the amino acid sequence of interleukin
CC (IL)-6R-alpha domain. The protein is used in the course of the invention.
CC The specification describes cytokine antagonists comprising only the
CC extracellular domain of the specifically-determining component of
CC the cytokine receptor and the extracellular domain of a cytokine
CC antagonist. The amino acid sequence of the IL-6R-alpha domain
CC is an interleukin (IL)-1, IL-2, IL-3, IL-4, IL-5 or IL-15).
CC granulocyte macrophage colony-stimulating factor (GM-CSF),
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional
CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.

SO Sequence 360 AA:

Query Match 100.0%; Score 102; DB 20; Length 360;
Best Local Similarity 100.0%; Pied. No. 2, 6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 PRSTSLTKRAVLIAKPKRNS 21
|||||
Db 136 PRSTSLTKRAVLIYRKFGS 156

RESULT 15
AA972199
CD AAI921299 standard; protein; 360 AA.
XX
XX AMY921299;
XX
D7 01-MUG-2000 (first entry)
XX
DE Soluble human IL-6-R-alpha.
XX
XX Soluble IL-6-R-alpha; cytokine; antagonist; CNTF receptor;
XX fusion protein; cytosolic; immunomodulator; osteopontic.
OS Homo sapiens.
XX
PN W0200018937-A2.
PD
PD 06-APR-2000.
PP
PP 22-SEP-1995; 99MO-US22045.
PR
PR 25-SEP-1996; 98US-0101858.
PR 19-MAY-1995; 99US-0313942.
XX
XX (REGG-) REGENERON PHARM INC.
PA
PI Stahl N, Yancopoulos GD;
PT
PT WP1; 2000-233165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX
XX Example 4; Fig 15; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC signal alpha specifically determining component of the receptor
 CC sequence alpha specifically determining component of the receptor
 CC (beta-1) and the beta-1 receptor (beta-1) are combined to
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (beta-1:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (cellary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC contrast to the known heterodimer, the alpha and beta receptor
 CC consisting of the ligand, its alpha receptor and its beta receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specifically determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native receptors. The heterodimers are useful for the treatment of
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

XX
 SQ Sequence 360 Aa;

Query Match 100.0%; Score 102; DB 21; Length 360;
 Best Local Similarity 100.0%; Pred. No. 2; 6e-09;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLVKRFKONS 21

DB 136 PRSCPALCKKAVLVKRFKONS 156

Search completed: December 19, 2001, 16:19:34
 Job time: 359 sec

F:387-468/Domain: Intracellular #status predicted <INT>
 F:47-96/Dsulfide bonds: #status predicted
 F:55-95/221,245,350/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 102; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1,5e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 PESTPTPTKAVILVRFKFN 156

RESULT 2

JL0144

Interleukin-6 receptor precursor (clone lambda p1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
 C:Accession: J01044
 R:Sigita, T.; Tschapek, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A:Title: Functional murine Interleukin-6 receptor with the intracisternal a particle get
 A:Reference number: J01044; MUID:90278354
 A:Accession: J01044
 A:Residues: 1-440 <SDG>
 A:Molecule type: mRNA
 A:Cross-references: GB:X51916; NID:953548; PIDN:CAA36238.1; PID:953549
 C:Keywords: cytokine receptor; transmembrane protein
 C:Keywords: cytokine receptor; transmembrane protein
 F:117-306/Domain: signal sequence #status predicted <SIT>
 F:20-462/Domain: extracellular #status predicted <EXT>
 F:40-94/Domain: immunoglobulin homology <IMH>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 56.9%; Score 56; DB 2; Length 440;
 Best Local Similarity 52.1%; Pred. No. 0.054;
 Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

DB 132 PESTPTPTKAVILVRFKFN 152

RESULT 3

JL0145

Interleukin-6 receptor precursor (clone lambda 301) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
 C:Accession: J01045; S14543
 R:Sigita, T.; Tschapek, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A:Title: Functional murine interleukin-6 receptor with the intracisternal a particle get
 A:Reference number: J01045; MUID:90278354
 A:Accession: J01045
 A:Residues: 1-460 <SDG>
 A:Molecule type: mRNA
 A:Status: nucleic acid sequence not shown
 A:Cross-references: GB:X51915; NID:949275; PIDN:CAA36237.1; PID:949276
 R:Rifollito, M. T.; Clibberio, G.; Dentis, L.
 submitted to the EMBL Data Library, 1990
 A:Description: Cloning and expression of murine IL-6 receptor.
 A:Reference number: S14543
 A:Accession: S14543
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Cross-references: GB:X51916; NID:953548; PIDN:CAA36238.1; PID:953549
 A:Cross-references: EMBL:X51802; NID:952692; PIDN:CAA37810.1; PID:952693
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin

C:Keywords: cytokine receptor; transmembrane protein
 F:117-306/Domain: signal sequence #status predicted <SIT>
 F:20-462/Domain: extracellular #status predicted <EXT>
 F:40-94/Domain: immunoglobulin homology <IMH>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 56.9%; Score 56; DB 2; Length 460;
 Best Local Similarity 52.1%; Pred. No. 0.054;
 Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

DB 132 PESTPTPTKAVILVRFKFN 152

RESULT 4

A37986

Interleukin-6 receptor precursor - rat
 N:Alternate names: IL-6 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C:Accession: A37986
 R:Kishimoto, T.; Tschapek, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
 J. Exp. Med. 171, 2001-2009, 1990
 A:Title: Molecular cloning, characterization and functional expression of the rat IL-6
 A:Reference number: A37986; MUID:91060502
 A:Accession: A37986
 A:Molecule type: mRNA
 A:Residues: 1-462 <RAD>
 A:Cross-references: GB:X05687; GB:X05688; NID:920492; PIDN:AAA1431.1; PID:920492
 C:Keywords: cytokine receptor; transmembrane protein
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin
 F:117-306/Domain: signal sequence #status predicted <SIT>
 F:20-462/Domain: extracellular #status predicted <EXT>
 F:40-94/Domain: immunoglobulin homology <IMH>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane #status predicted <TRA>
 F:386-462/Domain: intracellular #status predicted <INT>
 F:47-92/Dsulfide bonds: #status predicted

Query Match 54.9%; Score 56; DB 1; Length 462;
 Best Local Similarity 52.1%; Pred. No. 0.112;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

DB 132 PESTPTPTKAVILVRFKFN 152

RESULT 5

B82609

Hypothetical protein XP2042 [Imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: B82609
 R:Ramanojulu, V.; The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
 uence Analysis, 1999
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: B82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A53928 below
 A:Accession: B82609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <SDH>
 A:Cross-references: AB:AF004021; GB:A2003849; NID:99107139; PIDN:AF68844.1; GSPB:GN
 A:Cross-references: EMBL:AF004021; NID:99107139; PIDN:AF68844.1; GSPB:GN
 R:Stinson, A.J.G.; Reibach, F.C.; Arruda, P.; Abreu, F.A.; Aceituno, M.; Alvarez, R.
 B. J. Phylog. 1995
 B:Triones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer


```

C:Genetics:
A:Gene: SPDB:SPDC1271.15c
A:Map position: 2
A:Gene: nuclear
C:Keywords: translation initiation factor IF-2; translation elongation factor Tu hom
F:172-283/Domain: translation elongation factor Tu homology <RTU>

Query Match 42.28; Score 43; DB 2; Length 686;
Best Local Similarity 50.04; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 PRSPSTTAAVLYAKRON 20
||||| ||||| ||||| |||||
Db 84 PRSPSTLTPLPAVLSVAFPM 103

RESULT 10
Hypothetical protein R05F9.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: T16693
C:Accession: T16693; T27894
R:Hallsworth, K.
A:Description: The sequence of C. elegans cosmid R05F9.
A:Reference number: 218559
A:Accession: T16693
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-919 <HA>
A:Cross-references: EMBL:U01533; NID:g1109807; PID:g1109820; PIDN:AAAB3174.1; CESP:R05F9
submitted to the EMBL Data Library, June 1995
R:Hallsworth, K.
A:Description: The sequence of C. elegans cosmid ZK546.
A:Reference number: Z20437
A:Accession: T12894
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-575 <HA>
A:Cross-references: EMBL:U29380; PIDN:AAAB6743.1; CESP:ZK546.10
A:Experimental source: strain Bristol NZ
C:Genetics:
A:Gene: CESP:R05F9.12; CESP:ZK546.10
A:Intons: 31/3; 174/3; 329/3; 524/3; 575/2; 607/2; 645/2; 739/1; 816/3
C:Superfamily: Lysosomal alpha glucosidase; sucrase/isomaltase homology; trefoil homology

Query Match 42.28; Score 43; DB 2; Length 919;
Best Local Similarity 72.74; Pred. No. 43;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 PRSPSTTTAKA 11
||||| ||||| ||||| |||||
Db 744 PRQPSSTTTA 754

RESULT 11
T31419
Cyclic beta 1-2 glucan synthetase - Brucella abortus
C:Species: Brucella abortus
C:Date: 29-Oct-1999 #sequence_rev150 29-Oct-1999 #text_change 07-Dec-1999
C:Accession: T31419
R:Baron de Iannino, N.; Britnes, G.; Tolmashy, M.; Ugalde, R.A.
J. Bacteriol. 180, 4392-4400, 1998
C:Keywords: molecular cloning and characterization of cgs, the Brucella abortus cyclic beta
glucan synthetase
A:Reference number: Z21023; MUID:59389650
A:Accession: T31419
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A:Residues: 1-2831 <IM0>
A:Cross-references: EMBL:AF047823; NID:g3551790; PID:g3551791; PIDD:AAC34747.1
C:Genetic loc:
G:Gene: cgs
Query Match      42.2%; Score 43; DB 2; Length 2831;
Best local Similarity 60.0%; Pred. No. 1,5e+02;
Matches 1; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
OY 1 PRSTSLT-KAVLYNRF 18
    |||||
Db 678 PRVPSLTGDASFLQANF 697

RESULT 12
T45577
probable dddpd4-keto-6-deoxyhexose reductase [imported] - Streptomyces violaceoruber
C:Species: Streptomyces violaceoruber
C:Accession: U04-F08-6527 sequence_revision 04-Feb-2000 text_change 11-May-2000
R:Chromosome: K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; F
Chem. Biol. 5, 647-659, 1998
A:Title: The granaticin biosynthetic gene cluster of Streptomyces violaceoruber Tn23.
A:Reference number: Z23045; MUID:95051446
A:Accession: T46527
A>Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1529
A:Cross-references: EMBL:AJ011900; PIDD:CAA09643.1
A:Experimental source: strain Tu22
C:C Genetics:
A>Note: gra-orf22

Query Match      41.2%; Score 42; DB 2; Length 304;
Best local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 RSTPSLTTRKAVLVNR 16
    | : : : : |
Db 42 RGAGVTTRANDVLR 56

RESULT 13
T21460
Theoretical protein F28C6.2 - Ctenorhabdittis elegans
C:Species: Ctenorhabdittis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 text_change 15-Oct-1999
C:Accession: T21460
R:Burton, J.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19429
A:Accession: T21460
A>Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 255
A:Cross-references: EMBL:L268315; PIDD:CAA2668.1; GSPDB:GN00020; CBSP:F28C6.2
A:Experimental source: clone F28C6
C:C Genetics:
A:Gene: CBSP:F28C6.2
A:Map position: 2
A:Introns: 81/3; 278/2; 365/2

Query Match      51.2%; Score 42; DB 2; Length 535;
Best local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 2 RSTPSLTRKAVLVNKKON 20
    || : : : ||| ||
Db 418 RSVLSITRVAIVLKTEKTON 436

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RESULT 14

AS6731
chromatin assembly factor I p150 chain - human
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000
C:Accession: AS6731
R:Kaufman, P.D.; Kobayashi, R.; Kessler, N.; Stillman, B.
Call 81, 1105-1114, 1995
A:Title: The p150 and p60 subunits of chromatin assembly factor I: a molecular link betw
A:Reference number: AS6731; MID:95323966
A:Accession: AS6731
A:Status: preliminary
A:Residues: 1-938 <NA>
A:Molecule type: mRNA
A:Cross-references: GB:U20979; NID:9882257; PID:AAA6736.1; PID:9882258

Query Match

Best Local Similarity 41.2%; Score 42; DB 2; Length 938;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PRSTPSLTAKAVLVKRFONS 21

DB 186 PRSCPELTSGPRMCPKREDS 206

RESULT 15

denzin-180 - rat
N:Alternate names: postsynaptic density protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C:Accession: T31434
R:Appelton, M.L.; Moon, I.S.; Kennedy, M.B.
Call 15, 6893-6895, 1999
A:Title: Characterization of denzin-180, a new brain-specific synaptic protein of the o
A:Reference number: Z21033; MID:96421675
A:Accession: T31434
A:Status: preliminary; translated from cDNA/DBJ
A:Molecule type: mRNA
A:Residues: 1-1495 <AA>
A:Cross-references: EMBL:U66707; NID:91657757; PID:91657758; PID:AA052881.1
A:Residual source: strain Sprague Dawley
C:Function:
A:Description: supposed to participate in specific adhesion between presynaptic and post

Query Match

Best Local Similarity 41.2%; Score 42; DB 2; Length 1495;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 KAVLVKRFONS 21

DB 1473 KAVLVKRFONS 1484

Search completed: December 19, 2001, 16:22:38
Job time: 458 sec

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F:387-468/Domain: intracellular status predicted <INT>
F:47-96/Dsulfide bonds: status predicted
F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) status predicted

Query Match 100.0% Score 146; DB 1; Length 468;
Best Local Similarity 100.0% Pred. No. 1,se-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMWGRTSPSTLTKAVLLVNRKQNSPAED 28
DB 133 EMWGRTSPSTLTKAVLLVNRKQNSPAED 160
|||||

RESULT 2
JL0144
Interleukin-6 receptor precursor (clone lambda p1) - mouse
C/Species: Mus musculus (house mouse)
C/Accession: J1-Dec-1991 #sequence,Evolution 31-Dec-1991 #text,Change 21-Jan-2000
R/Accession: J10144; T.: Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J:Exp Med. 177, 2001-2009, 1990
A:Title: Functional murine interleukin-6 receptor with the intracisternal a particle gene
A:Reference number: J10144; MUID:90278334
A:Accession: J10144
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Accession: J10144
A:Cross-references: GB:X51976; NID:953548; P1DN:CA36238.1; P1D:953549
C/Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunog
C/Keywords: cytokine receptor; transmembrane protein
F:10-44/Domain: signal sequence status predicted <SIG>
F:20-44/Product: interleukin-6 receptor status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IM>
F:117-368/Domain: cytochrome receptor homology <CR>
F:358-368/Domain: transmembrane fold status predicted <TRA>

Query Match 49.3% Score 72; DB 2; Length 440;
Best Local Similarity 58.3% Pred. No. 0,0037;
Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 EMWGRTSPSTLTKAVLLVNRKQNS 24
DB 129 EMWGRTSPSTLTKAVLLVNRKQNT 152

RESULT 3
JL0145
Interleukin-6 receptor precursor (clone lambda 301) - mouse
C/Species: Mus musculus (house mouse)
C/Accession: J1-Dec-1991 #sequence,Evolution 31-Dec-1991 #text,Change 21-Jan-2000
R/Single, T.: Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J:Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin-6 receptor with the intracisternal a particle gene
A:Reference number: J10144; MUID:90278334
A:Accession: J10145
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Accession: J10145
A:Cross-references: GB:X51975; NID:949725; P1DN:CA36237.1; P1D:949726
C/Experimental source: clone lambda 301
R:Florillo, M.T.; Gilberto, G.; Dentle, L.
Submitted to the EMBL Data Library, July 1990
A:Description: Cloning and expression of murine IL-6 receptor.
A:Reference number: J14543
A:Accession: J14543
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Accession: J14543
A:Cross-references: EMBL:X53802; NID:952692; P1DN:CA37810.1; P1D:952693
C/Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunog

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C:keyWords: cytokine receptor; status predicted <SIG>
E:20-460/Product: interleukin-6 receptor; status predicted <KAT>
F:117-306/Domain: transmembrane homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match          49.3%   Score 72: DB 2: Length 460:
Best Local Similarity 58.3%   Pred. No. 0.0035:
Matches 14: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

OY      1 EMSPSTPTTKRAVLAKRNKS 24
        |||#####||| : :
Db       129 EMRSPSTPTTKRAVLFKNKIPT 152

RESULT      4
Interleukin-6 receptor precursor - rat
N:Alternate names: IL-6 receptor
C:Species: Rattus norvegicus (Norway rlt)
C:Place: 30-Jun-1993 #sequence,revision 30-Jun-1993 #text,change 22-Jun-1999
A:Accession: A37986
R:Baumann, H.; Baumann, H.; Roy, G.H.
J.Mol.Biol. Comp. 3:595-598(1993)
A>Title: Molecular cloning, characterization and functional expression of the rat lly
A:Reference number: A37986; MUID:91060502
A:Accession: A37986
A:Molecule type: mRNA
A:Seqidns: 1:462 <RNA>
A:Cross-references: GB:MS8587; GS:J05658; NID:g704921; PIDD:AAA4431.1; PID:g704922
C:Comment: After binding IL-6, this chain associates with the receptor tyrosine kinase
C:Subcellular location phase cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-462/Product: interleukin-6 receptor #status predicted <KAT>
F:20-362/Domain: extracellular #status predicted <EXT>
F:40-94/Domain: immunoglobulin homology <IMH>
F:117-306/Domain: cytokine receptor homology <CRS>
F:363-385/Domain: transmembrane #status predicted <TRA>
F:306-348/Domain: intracellular #status predicted <INT>
F:47-92/Dissulfide bonds: #status predicted

Query Match          47.9%   Score 70: DB 1: Length 462:
Best Local Similarity 54.2%   Pred. No. 0.008:
Matches 13: Conservative 3: Mismatches 8: Indels 0: Gaps 0:

OY      1 EMCHREPSPTTKAVLVKRNKS 24
        |||#####||| : :
Db       129 EMHSSTPTTKAVLFAFKNIPT 157

RESULT      5
hypothetical protein XF2042 [imported] - xylella fastidios (strain 9a5c)
C:Date: 16-Aug-2000 #sequence,revision 20-Aug-2000 #text,change 20-Aug-2000
C:Accession: DB82609
R:anonymous. The Xylella fastidiosa Consortium of the Organisation for Nucleotide Seq
Native 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB2515; MUID:20365917
A>Note: for a complete list of authors see reference number A53328 below
A:Accession: DB82609
A:Status: predicted
A:Subcellular location: cytoplasm
A:Residues: 1:242 <STM>
A:Cross-references: GB:AB0004021; GB:AB003849; NID:g9107139; PIDD:NMF8484.1; CSPDB:AGNO40421;
A:Experimental source: strain 9a5c
R:Stimpson, A.J.G.; Belnach, F.C.; Arvida, P.; Abreu, F.A.; Acencio, M.; Alvareznga, R.;
Ritones, M.R.S.; Bueno, M.R.P.; Canarajo, A.A.; Canarajo, L.E.A.; Carraro, D.M.; Carreir
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Q1      1  EKHGRSTSLTKAVLLVKKQN 23
      10  11 12 13 14 15 16 17 18 19 20 21 22
      10  11 12 13 14 15 16 17 18 19 20 21 22
Db      374  QMNPKRDSMTKYNNMLTGRQN 396

PROTEIN      9
T06793
N:Alternate names: rust resistance kinase Lr10
C:Protein description: Aestivum (Common wheat)
C:Spec.23-Apr-1999 #sequence=151510 23-Apr-1999 #text_change 11-May-2000
C:Accession: T06793
R:Reiller, C.; Schachermayr, G.; Keller, B.
Plant J. 11, 45-52, 1997
A:Title: A novel class of receptor-like kinase mapping to the Lr10 locus in wheat.
A:Reference number: Z15819; MWID:91717795
A:Accession: T06793
A:Status: preliminary; translated from CB/EML/DD53
A:Accession: T06793
A:Positives: 4635 <PID>
A:Cross-references: EML:U51330; NID:g1680685; PID:AA049629.1; PID:g1680666
C:Experimental source: leaf
C:Genetics:
A:Gene: LrK10
A:Map position: 1
A:Insertions: 272A; 280J
A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

```

```

Query Match Similarity      33.6%  Score 49; DB 2;  Length 636;
Best Local Similarity      34.8%  Pzed. No. 19;
Matches      8;  Conservative      6;  Mismatches      9;  Indels      0;  Gaps      0;

Oy      1  ECHGRTDGLTAVLVATLVKKKN 23
      ||| ||||| |||
Db      597  QMNRPRSPMTKYVMWTRGLQS 619

RESULT 10
S559861      3 band 3 anion transport protein isoform b - rainbow trout
C:Accession: S559861
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
R:Flavet, B.; Gabilliat, N.; Borgeese, F.; Molais, R.
EMBO J. 14, 5158-5169, 1995
A:Title: Expression of band 3 anion exchanger induces chloride current and taurine trans-
A:Reference number: S559861; MIMD:960800151
A:Status: preliminary
A:molecule type: mRNA
A:residues: 1-912 <FRT>
A:cross-references: EMBL:Z50948; NID:91004316; PTDN:CA90701.1; PID:91004317
A:superfamily: band 3 anion transport protein

```

```

Query Match      33.6%; Score 49; DB 2; Length 912;
Best Local Similarity 34.6%; Pwd. No. 29;
Matches      9; Conservative      7; Mismatches      10; Indels      0; Gaps      0;

Oy      1 EMGRSTSLTKAVLYKRNQNSPAV 26
      :|||      |||:::      |||:::
      104 KMGCSVSTFEKSLQIKRLKLTSGA 129
Db

```

RESULT 11
S24318
band 3 anion transport protein - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)

```

C:/Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text-change 20-Aug-1999
A:/Accession: S24318, S36083, S22173
R:/Rebner, S.; Michel, P.; Rüdolf, V.; Appelhaus, H.
B:/Date: J. 285, 17-23, 1992
A:/Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derived
A:/Accession: S24318, M01D9234456
A:/Molecule type: mRNA
A:/Residues: 1-918 <HUE1>
A:/Cross-references: EMBL:X61699
A:/Accession: S36083
A:/Molecule type: protein
A:/Residues: 71-89;94-114;570-588 <HUE2>
A:/Title: Band-3 protein from rainbow trout erythrocytes submitted to the EMBL data library, August 1991
A:/Reference number: S22173
A:/Accession: S22173
A:/Molecule type: mRNA
A:/Residues: 1-304, 'G', 306-918 <APP>
A:/Cross-references: EMBL:X61699; NID:g64308; PID:g64309
C:/Superfamily: band 3 anion transport protein
C:/Keywords: erythrocyte; transmembrane protein

Query Match      33.6%  Score 49.7  DB 2:  length 918:
Best Local Similarity 34.6%  Pred. NO. 29:
Matches      9:  Conservative      7:  Mismatches
                                10:  Indels
                                0:  Gaps
                                0:

QY      1 EWGPRSTSLTKRAVLIVKRFQNSPA 26
      |||||  ||:::  ||  ::  :
13b    110 KWGSHNSVILFRSLDLQKLNKSTGSA 135

```

RESULT 12
 A:71056
 C:probable 5'-methylthioadenosine phosphorylase - *Pyrococcus horikoshii*
 C:Species: *Pyrococcus horikoshii*
 C:Date: 14-Aug-1998 [sequence revision](#) 14-Aug-1998 [text change](#) 20-Jun-2000
 C:Accession: A71056
 R:Amagasaki, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Sato, M.; Ohkura, I.; Funahashi, T.; Tanaka, T.; Kidono, T.; Yamazaki, J.; Kusuda, M.; Ogo, D.N. *Nes. J. Biochem.* 1998
 A:Accession: A71056
 A:Accession: A71000; MIMD:98344137
 A:Accession: A71056
 A:status: preliminary; nucleic acid sequence not shown; translation not shown
 A:molecule type: DNA
 A:Residues: 1-265 <KAM>
 A:Cross-references: GB:AB000005; NID:9326132; PDB:1BA0243.1; PID:93257560
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:GenBank:
 A:Gene: PH143
 A:Superfamily: 5'-methylthioadenosine phosphorylase

```

Query Match      32.9%  Score 48:  DB 2:  Length 265:
Best Local Similarity 41.7%:  Prod. No. 10:
Matches 10;  Conservative 5;  Mismatches 9;  Indels 0;
Gaps 0:

QY      5  KSPSTSLTKAVILVKNQNSPAED 28
      |  :| :||| :| :| :| :| :|
Db      235 RETAILATIKAIPLIKERNCCDND 258

```

RESULT 13
T24637
hypothetical protein T07C12.11 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Access: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24637
R:McMurray, A.
submitted to the EMBL Data Library, June 1996

```

A:Reference number: 219916
A:Accession: T42637
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1268 <init>
A:Experimental source: EMBL-473975; PIDN:CAA9280.1; GSPDB:GND0023; CESP:T07C12.11
A:Experimental source: clone T07C12
A:Genes: CESP:T07C12.11
A:Map position: 5
A:Introns: 118/3; 180/3; 227/2

Query Match          32.9%  Score 48;  DB 2;  Length 265;
Best Local Similarity 47.8%  Prod No 11;
Matches 11;  Conservative 4;  Mismatches 9;  Indels 0;  Gaps 0;

OY      6  STPSLTAAVLKRRQNSPAD 38
      ||| ||| ||| ||| |||
Db      222  SEPVLLICVLFVERIQSPQE 244

RESULT 14
T48903
wax synthase [Imported] ; Simmondsia chinensis
C:Species: Simmondsia chinensis
C:Date: 02-Jun-2000 #sequence revision 02-Jun-2000 #text_change 02-Jun-2000
A:Accession: T48903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1352 <init>
A:Cross-References: EMBL:AF149919; PIDN:AAD3041.1

Query Match          32.9%  Score 48;  DB 2;  Length 352;
Best Local Similarity 40.0%  Prod. No. 14;
Matches 12;  Conservative 4;  Mismatches 10;  Indels 4;  Gaps 1;

OY      3  GNSPTST---TKAVLLKRRQNSPAD 28
      ||| ||| ||| ||| |||
Db      85  GFLNPSLSLHFTSTLLPLTKRQDSND 114

RESULT 15
Q08C55
Hypothetical 73.3% protein (mreb-acbB intergenic region) - Escherichia coli (strain K-12)
C:Feature names: Hypothetical protein 102 (envs 5' region)
C:Date: 31-Mar-1990 #sequence revision 30-Sep-1997 #text_change 26-Aug-1999
A:Accession: F63117; B1843; F60032
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Sisco, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Accession: F63117
A:Cross-References: N64720; M01D:91426617
A:Abstract: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1646 <BLAT>
A:Cross-References: GB:AA000404; GB:U00096; NID:92367207; PIDN:AA076284.1; PID:gi789650.0;
A:Experimental source: strain K-12, substrain MG1655
R:Boi, M.; Machi, M.; Ishino, F.; Tomoka, S.; Ito, M.; Sakagami, Y.; Suzuki, A.; Matsui, A.;
A:Title: Determination of the DNA sequence of the mreb gene and of the gene products of
A:Accession number: A91887; M01D:8908079
A:Accession: B1843
A:Molecule type: DNA
A:Residues: 545-646 <D01>

```

```

A:cross-references: GB:M2055; NID:q446887; PIDN:AAA83890.1; PTD:gil128956
A:Experimental source: strain K12
C:Genetics:
A:Gene: yhaA
A:Map position: 71 min
C:Superfamily: Escherichia coli hypothetical 73-3K protein (meab-acb intergenic regi
Query Match          32.2%   Score 47; DB 1; Length 646;
Best local similarity 41.7%; Pred. No. 40;
Matches 10; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
QY      1 EMGFASTSLTKAVLLAKFQNS 24
        II I I I I I I I I I I
Db      190 EMPRSSALDT---LMEIQKN 209

```

GeneCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:15 ; Search time 48.45 Seconds
(without alignments)

15,892 Million cell updates/sec

Title: US-09-202-104a-5
Perfected score: 102
Sequence: 1 PRSTPSITKNAVLKRRKMS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Query	Score	Match	Length	DB ID	Description
1	102	100.0	468	1	IL6A_HUMAN	P08887 homo sapien
2	89	87.3	467	1	IL6A_PIG	O18796 sus scrofa
3	58	85.9	460	1	IL6A_MOUSE	P22772 mus muscula
4	58	85.9	460	1	IL6A_MOUSE	P22772 mus muscula
5	46	45.1	328	1	PMEL_RHHA	O00972 kluyveromy
6	43	42.2	586	1	IF2K_ARATH	O43867 arabidopsis
7	43	42.2	586	1	IF2K_ARATH	O43867 arabidopsis
8	43	42.2	586	1	CAP2_MOUSE	O43299 amaranthus
9	42	40.2	1028	1	BCAL_MOUSE	O47077 enterobacte
10	41	40.2	1234	1	PR2A_MOUSE	P22043 tomatoblac
11	39	39.2	119	1	YF6A_HYVE	P22043 tomatoblac
12	39	39.2	119	1	YF6A_HYVE	P22043 tomatoblac
13	40	39.2	179	1	PRH_CHHR	O08406 chlamydia
14	40	39.2	190	1	PRPC_MOUSE	P35245 muscivis
15	40	39.2	841	1	PR2A_HUMAN	O15127 homo sapien
16	40	39.2	914	1	AT5E_HUMAN	O94823 homo sapien
17	40	39.2	1038	1	CINE_YEAST	P27895 saccharomyc
18	40	39.2	2870	1	NDBE_ARATH	P20471 thiazobium
19	38	38.2	35	1	AT5E_HUMAN	O94823 homo sapien
20	38	38.2	35	1	AT5E_HUMAN	O94823 homo sapien
21	38	38.2	192	1	CHRP_DROPS	P16565 drosophil
22	38	38.2	194	1	CHRP_DROPS	P16565 drosophil
23	38	38.2	330	1	PRPC_MOUSE	O05534 emeritella
24	38	38.2	342	1	YF6A_HYVE	P40004 saccharomyc
25	38	38.2	457	1	PR2A_HUMAN	O15127 homo sapien
26	38	38.2	464	1	PR2A_HUMAN	O15127 homo sapien
27	38	38.2	960	1	PR2A_HUMAN	O15127 homo sapien
28	38	38.2	960	1	PR2A_HUMAN	O15127 homo sapien
29	38	38.2	1176	1	NIR_NICOT	P18681 nicotiana
30	38	38.2	1517	1	YF6A_HYVE	O10250 schizosach
31	38	38.2	2774	1	MAPA_RAT	P24926 rattus norv
32	38.5	37.7	225	1	YF6A_HYVE	O10250 schizosach
33	38.5	37.7	395	1	SOC_DROME	P49415 drosophila

RESULT	1	STANDARD:	PRT:	468 AA.
ID	IL6A_HUMAN			
AC	P08887	016202		
NC	01-NOV-1988 (Rel. 09, Created)			
DI	01-NOV-1988 (Rel. 09, Last sequence update)			
DE	20-NOV-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)			
OS	(CD126 ANTIGEN).			
OS	IL6R.			
OS	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OS	Mammalia; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID:9606;			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
EX	MEDLINE=88305347; PubMed=316546;			
RA	Yamasaki K., Hirano T., Hirata Y., Yawata H., Kawashita Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RA	Yamasaki K., Hirano T., Hirata Y., Yawata H., Kawashita Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	Structure and functional studies on the human Interleukin-6 (IL-6) receptor.			
RT	Science 241:825-828(1988).			
RL	[2]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
EX	MEDLINE=9136983; PubMed=1872801;			
RA	Schoolnik H., Sloyan T., Lanz D., Schmitz H., Hirano T.,			
RA	Kishimoto T., Heinrich P.C., Rose-John S.;			
RA	Structural and functional studies on the human hepatic Interleukin-6			
RT	receptor. Molecular cloning and overexpression in Hep2 cells.?			
RT	Biochem. J. 277:659-664(1991).			
RL	[4]			
RP	SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).			
EX	MEDLINE=94333499; PubMed=8056053;			
RA	Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,			
RA	Matsumoto A., Yamamoto N., Yamamoto N.			
RT	Soluble Interleukin-6 receptors released from T cell or			
RT	granulocyte/macrophage cell lines and human peripheral blood			
RT	mononuclear cells are generated through an alternative splicing			
RT	mechanism.?			
RT	Eur. J. Immunol. 24:1945-1948(1994).			
RL	[5]			
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.			
EX	MEDLINE=95167486; PubMed=10065782;			
RA	Cole A.R., Hall N.R., Tretelein H.R., Eddes J.S., Reid G.E.,			
RA	*Oligosaccharide transferase.?			
RA	*Oligosaccharide transferase.?			
RT	extracellular domain of the human Interleukin-6 receptor.?			
RT	J. Biol. Chem. 274:7207-7215(1999).			
RL	[6]			
RP	MUTAGENESIS.			

ALIGNMENTS

34	38.5	37.7	419	1	VS48_TBRVC	P22048 tomatoblac
35	38	37.3	180	1	PRH_CHHR	O08406 chlamydia P
36	38	37.3	218	1	Y3B1_MYCBE	P47621 mycoblasma
37	38	37.3	403	1	YDHC_ECOLI	P37597 escherichia
38	38	37.3	424	1	VS48_TBRVC	P22050 tomatoblac
39	38	37.3	424	1	VS48_TBRVC	P22050 tomatoblac
40	38	37.3	424	1	VS48_TBRVC	P22050 tomatoblac
41	38	37.3	719	1	GROU_DROME	P16571 drosophila
42	38	37.3	926	1	YF6A_HYVE	O10250 schizosach
43	38	37.3	960	1	CAP1_MOUSE	P29195 sorghumbic
44	38	37.3	960	1	CAP1_MOUSE	P29195 sorghumbic
45	38	37.3	960	1	CAP2_SORBI	P29194 sorghumbic

RN [2]
 RP SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE=Liver;
 RE PubMed abstract of porcine interleukin 6 receptor.*
 RL Submitted (JUL-1997) to the EMBL/Genbank/DDBJ databases
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH LIGST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BT
 CC SIMILARITY: RECEPTOR OF TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: AF147881; MAF73109.1; -;
 DR EMBL: AF015116; MAF07916.1; -;
 DR HSSP: P16471; I8P3.
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003598; Ig_LHC.
 DR Pfam: PF00041; f03.1; Ig_L2.
 DR Pfam: PF00047; f9.1; -;
 DR SMART: SM00060; FN3.1.
 DR SMART: SM00408; IgC2.1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT CHAIN 1 19 BY SIMILARITY
 FT DOMAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 366 386 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193 BY SIMILARITY.
 FT DISULFID 121 136 BY SIMILARITY.
 FT DISULFID 137 152 BY SIMILARITY.
 FT CARBOHYD 165 176 N-LINKED (GLCNAAC. -) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAAC. -) (POTENTIAL).
 FT CARBOHYD 93 93 N-LINKED (GLCNAAC. -) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAAC. -) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAAC. -) (POTENTIAL).
 SQ CARBOHYD 467 AA; 51066 MW; A2808845EF21C502 CRC64;
 SQ SEQUENCE.

Query Match 87.3%; Score 89; DI 1; Length 467;
 Best Local Similarity 90.5%; Pred.No.2,3e-07;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRSPSTPTKAVILVKKFNS 21
 DB 136 PRSPSTPTKAVILVKKFNS 156
 RESULT 3
 ID IL6A_MOUSE STANDARD; PRT; 460 AA.

AC P22272;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 20-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 CC FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH LIGST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BT
 CC SIMILARITY: RECEPTOR OF TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: X51975; CAA36237.1; -;
 DR EMBL: X53802; CAA37810.1; -;
 DR PIR: J10144; J10144.
 DR PIR: J10145; J10145.
 DR PIR: S19343; S19343.
 DR MCD: M0105304; I166F.
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003598; Ig_LHC.
 DR Pfam: PF00041; f03.1; -;
 DR Pfam: PF00047; f9.1; -;
 DR SMART: SM00060; FN3.1.
 DR SMART: SM00408; IgC2.1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3.1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT CHAIN 1 19 BY SIMILARITY
 FT DOMAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 366 386 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 190 BY SIMILARITY.

[illegible]

```

OC   Viruses: ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC   Nepovirus.
OX   NCBI_TaxID=12277;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Edwards L., Meyer M., Graft C., Fritsch C.;
RT   Tomato leaf curl virus satollite RNAs.
RJ   J. Gen. Virol. 68:1823-1833(1987).
RN   [2]
RP   REVISIONS.
RA   Fritsch C.;
RT   Submitted (FEB-1988) to the EMBL/GenBank/DBJ databases.
OC   This SWISS-PROT entry is copyright. It is produced through a collaboration
OC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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OC   use by non-profit institutions as long as its content is in no way
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OC   or send an email to license@isb-sib.ch).
DR   EMBL; X05688; CAB59631.1; -.
DR   EMBL; D00143; BA000901.1; -.
DR   PIR; B27169; SAVTEE.
SQ   SEQUENCE 419 AA; 47992 MW; 78BD7B9C246C7CB CRC64;

Query Match          39.7%; Score 40.5; DB 1; Length 419;
Query Ident Similarity %; 5; Mismatches 18;
Matches 10; Conservative 5; Indels 4; Gaps 5;
QY   3 STS1-----TTXVAVLRFQNS 21
Db   121 STPAKTIQKFPESITLAKIQNS 144
      |||:  |||:|||||:|||||
RSUPRT 12
DCFC:ACTCA
ID   DCFC:ACTCA          STANDARD;          PRT;   134 AA.
AC   P20370;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2000 (Rel. 40, Last annotation update)
DE   4-CARBOXYMCDONALDSONE DECARBOXYLASE (EC 4.1.1.44) (CMD).
OS   Acetobacter calcoaceticus.
OC   Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC   Acetobacter.
OX   NCBI_TaxID=471;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   STRAIN-B9413; ADP1.
RA   Hartnett C., Meikle P.L., Ngai K.-L., Orston L.N.;
RT   RNA sequences of genes encoding Acetobacter calcoaceticus
RT   protoconatechase 3,4-dioxygenase: evidence indicating shuffling
RT   of genes and of DNA sequences within genes during their evolutionary
RT   divergence.
RT   J. Bacteriol. 172:955-966(1990).
RJ   1- CATALYTIC ACTIVATION OF 2-CARBOXY-5-OXO-2,5-DIHYDROFURAN-2-ACETATE =
RJ   - PATHWAY, THIRD STEP IN THE CATABOLISM OF PROTOCONATECHASE TO
RJ   SUCCINATE AND ACETYL COA IN THE BETA-RETRODIAPYCNATE PATHWAY.
OC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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OC   or send an email to license@isb-sib.ch).

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GN GPIIb2 OR PI(PLD2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
 OC ID: IPIB-9506;
 RN ID: IPIB-9506;
 RP SEQUENCE FROM N.A.
 RA Tissue: Liver;
 RA Tsang T.C., Fung W.-J.C., Levine J., Metz C.N., Davitz M.A.,
 RA Burns D.K., Huang K.-S., Kochan J.P.;
 RA Isolation and expression of two human glycosylphosphatidylinositol
 RA protein phosphatases (GPI-APs) cDNAs.
 RA J Biol Chem 267:13212-13219 (1992).
 CC FUNCTION: THIS PROTEIN HYDROLYSES THE INOSITOL PHOSPHATE LINKAGE
 CC IN PROTEINS ANCHORED BY PHOSPHATIDYLINOSITOL GLYCANS (GPI-ANCHOR)
 CC -!- CATALYTIC ACTIVITY: GLYCOPROTEIN PHOSPHATIDYLINOSITOL + H(2)O -
 CC PHOSPHATIDATE + GLYCOPROTEIN INOSITOL.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sdb-sdb.ch).
 CC
 CC EMBL: L11701; AAA36444.1; .
 CC MIM: 602515; .
 DR InterPro: IPR000413; Integrin_alpha.
 DR InterPro: IPR001028; Phosphatase_D.
 DR Pfam: PF01839; FG-GAP; 6.
 DR PRINTS: PR00718; PHIPILPASED.
 DR SMART: SM00191; Int_alpha; 5.
 DR PROSITE: PS00001; Phosphatase; Glycoprotein; Signal
 DR SIGNAL: 24
 FT CHAIN 25 841 BY SIMILARITY
 FT
 FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 326 326 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 502 502 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 592 592 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 605 605 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 660 660 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 841 AA: 92666 MW: 65666 PDA6A2D9DC2 CRG64;
 Oeury Match 39.2%; Score 40; DB 1; Length 841;
 Best Local Similarity 53.3%; Pred No. 75;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 5 PSLTAKAVLVKRFQ 19
 DB 231 PSLTAKAVLVKRFQ 245

Search completed: December 19, 2001, 16:26:15
 Job time: 570 sec

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Gencode version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:21 Search time 157.32 Seconds
(without alignments)
19.525 Million cell updates/sec

Title: US-09-202-104A-5

Perfect score: 102
Sequence: 1 PRSPSLTKNAVLLVKKRFS 21

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.invertebrate:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*

Prct. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	50	49.0	242	2	09PMU3
2	46	45.1	627	10	09AT00
3	44	43.1	371	11	09DS41
4	44	43.1	534	10	09PM74
5	44	43.1	572	4	09H171
6	44	43.1	1260	4	09H171
7	44	43.1	1260	4	09H171
8	44	43.1	1260	4	09H171
9	43	42.2	321	2	P74937
10	43	42.2	322	2	09KAV3
11	43	42.2	458	5	053624
12	43	42.2	519	5	021350
13	43	42.2	1054	12	09A159
14	43	42.2	1054	12	09A159
15	43	42.2	1054	12	09A159
16	42.5	41.7	701	10	09SRM4
17	42.5	41.7	957	10	09SRM4
18	42	41.2	296	11	09J142
19	42	41.2	304	2	09ZK37

ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	242 AA.
09PMU3				
AC	09PMU3-2000 (TRENDEL, 15, Created)			
DE	01-OCT-2000 (TRENDEL, 16, Last annotation update)			
DE	01-MAR-2001 (TRENDEL, 16, Last annotation update)			
GN	XP2042.			
OS	Xylella fastidiosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;			
OX	Xylella.			
OX	NCBI:TaxId=2371:			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=945C.			
MD	MEDLINE=20365717; PubMed=10910347;			
RA	Simpson A.J.G., Reinech F.C., Arruda P., Abreu F.A., Acencio M.,			
RA	Alvarenga R., Alves L.M.C., Ayala J.E., Bala G.S., Baptista C.S.,			
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,			
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter R.,			
RA	Colombo N.B., Colombo C., Costa F.F., Costa D.C., Costa Neto C.M.,			
RA	Costa Neto C.M., Costa Neto C.M., Costa Neto C.M., Costa Neto C.M.,			
RA	Fachinchi A.P., Ferreira A.J.S., Ferreira V.C.A., Ferriz J.A.,			
RA	Frada J.S., Franca S.C., Franco M.C., Prohne W., Purlan L.R.,			
RA	Gardier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Guiber A.,			
RA	Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,			
RA	Krieger J.E., Kurume E.E., Laifert F., Lambis M.R., Leite L.C.C.,			
RA	Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,			
RA	Lemos M.V., Martins E.M.L., Martins E.M.P., Matsukuma A.Y.,			
RA	Monck C.F.M., Miraca E.C., Miyaki C.Y., Montello-Vilarello C.B.,			
RA	Monck D.H., Negai M.A., Nascimento A.L.T.O., Neto L.E.S.,			
RA	Nahai A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,			
RA	de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,			
RA	Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Resqueiro J.B.,			
RA	Quagga V.E. Jr., Rodrigues P.G., Rodrigues P.G., Rodrigues P.G.,			
RA	de Silva A.C.R., de Silva A.M., de Silva F.R., Silva W.A. Jr.,			
RA	de Souza A.P., de Souza A.P., de Souza A.P., de Souza A.P.,			
RA	de Souza A.P., Terenzi M.F., Terenzi M.F., Terenzi M.F.,			
RA	Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,			

RA Zago M.A., Zatz M., Melandis J., Setubal J.C.;
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RA Nature 406:4021-435(2000). 1: -
 DL 406:4021-435(2000). 1: -
 KW Hypothetical protein: complete proteome.
 SO SEQUENCE 242 AA; 27518 MW; ACDDEBC09C9696 CRC64;

Query Match 49.0%; Score 50; DB 2; Length 242;
 Best Local Similarity 50.0%; Pred. No. 1.5;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLYRKFN 20
 I :::::::::::::::
 DB 45 PLILDSTSTAVLYRKFN 64

RESULT 2
 ID 09AT00 PRELIMINARY; PRT; 627 AA.
 AC 09AT00;
 DT 01-JUN-2001 (TRENDEL. 17, Created)
 DT 01-JUN-2001 (TRENDEL. 17, Last sequence update)
 DT 01-JUN-2001 (TRENDEL. 17, Last annotation update)
 DE LRR14.
 DE LRR14.
 CC Trillium aestivum (Wheat).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Penfield C., Penger A., Gellner K., Mast A., Keller B.;
 RA "Molecular Evolution of Receptor-Like Kinase Genes in Hexaploid Wheat.
 RA "Independent Evolution of Orthologs after Polyploidization and
 RA Mechanisms of Local Rearrangements at Paralogous Loci.";
 RL Plant Physiol. 125:1304-1313(2001).
 DL EMBL: AF325198; MAK20743.1; -
 SO SEQUENCE 627 AA; 70463 MW; 903BA872D19664FA CRC64;

Query Match 45.1%; Score 46; DB 10; Length 627;
 Best Local Similarity 45.0%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLYRKFN 20
 DB 599 PNRPSMTVYNNLGRFN 618

RESULT 3
 ID 09D541 PRELIMINARY; PRT; 371 AA.
 AC 09D541;
 DT 01-JUN-2001 (TRENDEL. 17, Created)
 DT 01-JUN-2001 (TRENDEL. 17, Last sequence update)
 DT 01-JUN-2001 (TRENDEL. 17, Last annotation update)
 DE 4930517G15SRK PROTEIN.
 GN 4930517G15SRK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=TESTIS;
 RA MEDLINE=2108560; PubMed=11217851;
 RA Arkava T., Hara A., Fukunishi Y., Yoshino M., Ishii Y.,
 RA Arkava T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iizawa M., Mishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki T., Gotohori T., Bono H., Kasukawa T., Saito K.,

RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA "Genome of *Caenorhabditis elegans*.";
 RA Nature 407:1518-1521(2000). 1: -
 DL 407:1518-1521(2000). 1: -
 KW Söhrli L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci F., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher N., Fujita M., Gariboldi M.F.,
 RA Gustinich S., Hall D., Holman M., Hume D., Ikenli K., Komatsu N.,
 RA Lyons E., Matsuoka Y., Nishikawa T., Okada M., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sosa T., Shihata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Borje A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 405:832-836(2000). 1: -
 DL 405:832-836(2000). 1: -
 DR MGI:1921953; 4930517G15SRK.
 SO SEQUENCE 371 AA; 42515 MW; BD0AD05BB21F556 CRC64;

Query Match 43.1%; Score 44; DB 11; Length 371;
 Best Local Similarity 41.2%; Pred. No. 24;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 4 TSPSLTTKAVLYRKFN 20
 I :::::::::::::::
 DB 258 TSPSLTTKAVLYRKFN 274

RESULT 4
 ID 09PM74 PRELIMINARY; PRT; 534 AA.
 AC 09PM74;
 DT 01-MAR-2001 (TRENDEL. 16, Created)
 DT 01-MAR-2001 (TRENDEL. 16, Last sequence update)
 DT 01-JUN-2001 (TRENDEL. 17, Last annotation update)
 DE SIMILARITY TO UNKNOWN PROTEIN.
 OS Arabidopsis thaliana (Mouse Streptophyta).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 CC Eusteroideae II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=COLDETERA.
 RA MEDLINE=510728; PubMed=9501997.
 RA Tabata S., Saito S., Kaneko T., Kotani H., Asanin E., Miyajima N.,
 RA "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RA Sequence features of the regions of 1,191,918 bp covered by seventeen
 RA physically assigned pl clones.";
 RL DNA Res. 4:401-414(1997).
 DL EMBL: AB007650; BAB08296.1; -
 DR EMBL: AB007650; BAB08296.1; -
 DR EMBL: PR02013; SM1B.1;
 DR SMART: SM00351; SM1B.1;
 SO SEQUENCE 534 AA; 59270 MW; 4331FP2343C18BD9D CRC64;

Query Match 43.1%; Score 44; DB 10; Length 534;
 Best Local Similarity 52.9%; Pred. No. 34;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 SPSPSLTTKAVLYRKFN 19
 I :::::::::::::::
 DB 95 SPSPSLTTSPNNKRFQ 111

RESULT 5
 ID 09HA71 PRELIMINARY; PRT; 572 AA.
 AC 09HA71;

RESULT 12
 ID Q21750 PRELIMINARY; PRT: 919 AA.
 AC Q21750; Q23517; (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HYPOHERICAL 103.3 KDA PROTEIN.
 GN R0559.12 OR ZK546.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodidae; Caenorhabditis.
 NC NCB1_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hallsworth K.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RC STRAIN=BRISTOL N2;
 RC SEQUENCE OF 1-575 FROM N.A.
 DR EMBL: Q23517; (1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U29380; AA68743.1; -;
 DR Interpro: IPR000322; Glyco_hydro.31.
 DR Pfam: PF01055; Glyco_hydro.31; 1.
 DR PROSITE: PS00129; GLYCOSYL_HYDROL_F31.1; 1.
 DR HYDROLASE 919 AA; 103314 MW; M48E718BF3685FC CRC64;
 SQ SEQUENCE

Query Match 42.2%; Score 43; DB 5; Length 919;
 Best Local Similarity 72.7%; Pred.No. 85;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PREPSLTTTKA 11
 DB 744 PRGPTSTTTTA 754

RESULT 13
 ID 094192 PRELIMINARY; PRT: 1744 AA.
 AC 094192;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHITIN SYNTHASE.
 GN CHS4.
 OS Paracoccidioides brasiliensis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Chaetothyriales; Dothideales; Dothiorales; Paracoccidioidales.
 NC NCB1_TaxId=121759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20210320; PubMed=10746225;
 RA Nino-Vega G.A., Munro C.A., San-Bias G., Gooday G.W., Gow N.A.;
 RT "Differential expression of chitin synthase genes during temperature-
 RT induced dimorphic transitions in Paracoccidioides brasiliensis.";
 RT Molecular Microbiology and Immunology 13:383-391 (2000).
 RN [2] Mycologia. 98:31-39(2000).
 RP SEQUENCE FROM N.A.
 RA Nino-Vega G.A., San-Bias G.;
 RT "Sequence analysis of the CHS4 gene of Paracoccidioides
 RT brasiliensis.";
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR Interpro: IPR001117; Chitinase.
 DR Interpro: IPR001173; Glycosyltransferase-2.
 DR Interpro: IPR001609; myosin head.
 DR Pfam: PF00063; myosin head; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.

SQ SEQUENCE 1744 AA; 193777 MW; DB7622D0A69F0705 CRC64;
 Query Match 42.2%; Score 43; DB 3; Length 1744;
 Best Local Similarity 44.4%; Pred.No. 1,6e+02;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 PREPSLTTTKAVLVYKRP 18
 DB 118 PLSTPSITVYALVYKRP 135

RESULT 14
 ID 010378 PRELIMINARY; PRT: 1967 AA.
 AC 010378;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE LARGE PROTEIN.
 GN Large protein.
 GN Large transitory yellowing virus.
 GN Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 NC NCB1_TaxId=59380;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Peng R., Luo Z., Zhou H.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RA EMBL: AB011257; B225160.1;
 SQ SEQUENCE 1967 AA; 223600 MW; DE70AB80A45FC776 CRC64;

Query Match 42.2%; Score 43; DB 12; Length 1967;
 Best Local Similarity 42.1%; Pred.No. 1,8e+02;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RSPSLTTTKAVLVYKRP 20
 DB 919 RSPDPVTEATCFIRFRKN 937

RESULT 15
 ID 085166 PRELIMINARY; PRT: 2831 AA.
 AC 085166;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CYCLIC BETA 1-2 GLUCAN SYNTHETASE.
 GN CGS.
 OS Bacillus abortus.
 OC Bacteria; Firmicutes; Bacillales; Bacilli; Rhizobiaceae group;
 OC Rhizobiaceae; Brucella.
 NC NCB1_TaxId=235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=519;
 RA MEDLINE=98399650; PubMed=921274;
 RA "Molecular cloning and characterization of cgs1 the Brucella abortus
 RT cyclic beta(1-2) glucan synthetase gene; genetic complementation of
 RT Rhizobium meliloti nody and Agrobacterium tumefaciens chyb mutants.";
 RT J. Bacteriol. 180:4392-4400(1998).
 DR EMBL: AF047823; AAC34747.1; -;
 SQ SEQUENCE 2831 AA; 316272 MW; 956A0399A57FC58 CRC64;

Query Match 42.2%; Score 43; DB 2; Length 2831;
 Best Local Similarity 60.0%; Pred.No. 2,6e+02;
 Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
 QY 1 PREPSLTTT--RAVLVYKRP 18

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      || ||||| : | | |
Db 678 PRVTPSLTGDEASFLORVF 697

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Search completed: December 19, 2001, 16:25:22
Job time: 547 sec

GenCode version 4.5
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OK protein - protein search, using sw model

Run on: December 19, 2001, 16:20:59 ; Search time 78.52 seconds
(without alignments)

6.018 Million cell updates/sec

Title: US-09-202-104a-5

Perfect score: 102

Sequence: 1 PPSPTSTTKAVLVKRRFGNS 21

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 212252 segs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents.AA*
1: /cgn2_6/pdata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/pdata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/pdata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/pdata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/pdata/2/1aa/PCUS.COMB.pep.*
6: /cgn2_6/pdata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	210	US-09-043-785-1	Sequence 1, App11
2	102	100.0	323	5171840-6	Patent No. 5171840
3	102	100.0	323	5480796-6	Patent No. 5480796
4	102	100.0	344	5171840-7	Patent No. 5171840
5	102	100.0	344	5480796-7	Patent No. 5480796
6	102	100.0	468	5171840-9	Patent No. 5171840
7	102	100.0	468	5480796-2	Patent No. 5480796
8	102	100.0	468	5480796-2	Patent No. 5480796
9	92	90.2	201	5171840-11	Patent No. 5171840
10	91	89.2	386	5171840-5	Patent No. 5171840
11	91	89.2	386	5480796-5	Patent No. 5480796
12	40	39.2	1038	US-09-441-782-4	Sequence 4, App11
13	38	37.3	211	US-07-915-966-4	Sequence 4, App11
14	38	37.3	211	US-08-653-154-4	Sequence 4, App11
15	38	37.3	211	US-08-150-802A-44	Sequence 44, App1
16	38	37.3	718	US-08-477-346-44	Sequence 44, App1
17	38	37.3	718	US-08-477-346-44	Sequence 44, App1
18	38	37.3	718	US-08-477-346-44	Sequence 44, App1
19	38	37.3	718	US-08-477-346-44	Sequence 44, App1
20	38	37.3	718	US-08-477-346-44	Sequence 44, App1
21	38	37.3	718	US-08-477-346-44	Sequence 44, App1
22	38	37.3	718	US-08-477-346-44	Sequence 44, App1
23	38	37.3	718	US-08-477-346-44	Sequence 44, App1
24	38	37.3	718	US-08-477-346-44	Sequence 44, App1
25	38	37.3	718	US-08-477-346-44	Sequence 44, App1
26	38	37.3	718	US-08-477-346-44	Sequence 44, App1
27	38	37.3	718	US-08-477-346-44	Sequence 44, App1

28	36	35.3	221	1	US-07-503-710-6	Sequence 6, App11
29	36	35.3	221	1	US-08-252-966B-8	Sequence 8, App11
30	36	35.3	221	1	US-08-222-658B-6	Sequence 2, App11
31	36	35.3	221	1	US-08-222-658B-6	Sequence 2, App11
32	36	35.3	648	1	US-08-321-356-4	Sequence 4, App11
33	36	35.3	985	2	US-08-804-326-41	Sequence 41, App1
34	36	35.3	4545	2	US-08-604-227C-14	Sequence 14, App1
35	36	35.3	4550	2	US-08-604-227C-8	Sequence 8, App11
36	36	35.3	4550	2	US-08-604-198-2	Sequence 2, App11
37	35.5	34.8	394	4	US-09-590-721-5	Sequence 5, App11
38	35.5	34.8	572	2	US-08-956-414B-1	Sequence 2, App11
39	35	34.3	113	2	US-08-313-227B-5	Sequence 2, App11
40	35	34.3	136	4	US-08-357-251-16	Sequence 16, App1
41	35	34.3	136	4	US-08-357-251-16	Sequence 16, App1
42	35	34.3	166	1	US-08-362-453-8	Sequence 8, App11
43	35	34.3	166	1	US-09-339-913B-79	Sequence 79, App1
44	35	34.3	189	1	US-08-026-79B-11	Sequence 11, App1
45	35	34.3	189	1	US-08-026-79B-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
US-09-043-785-1
Sequence 1, Application US/09043785

Patent No. 6172042

GENERAL INFORMATION: Judith

APPLICANT: BATH, Hubert

APPLICANT: REVEL, MICHEL

FILE REFERENCE: Chedath-1

CURRENT APPLICATION NUMBER: US/09/043,785

EARLIER FILING DATE: 1998-09-02

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

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EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

EARLIER FILING DATE: 1995-09-26

Query Match 100.0%; Score 102; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVLRKFN 21
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Db 136 PRSTPSLTTKAVLVLRKFN 156

RESULT 3
 5480796-6
 Patent No. 5480796
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION NUMBER: 298,694
 APPLICATION NUMBER: 298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 6:
 LENGTH: 323
 5480796-6

Query Match 100.0%; Score 102; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVLRKFN 21
 |||

Db 136 PRSTPSLTTKAVLVLRKFN 156

RESULT 4
 5171840-7
 Patent No. 5171840
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/298,694
 FILING DATE: 19-JAN-1989
 SEQ ID NO: 7:
 LENGTH: 344
 5171840-7

Query Match 100.0%; Score 102; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVLRKFN 21
 |||

Db 136 PRSTPSLTTKAVLVLRKFN 156

RESULT 5
 5480796-7
 Patent No. 5480796
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 FOR HUMAN B CELL STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 FILING DATE: 05/07/297,650
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 298,694

FILING DATE: 19-JAN-1989
 SEQ ID NO: 7:
 LENGTH: 344
 5480796-7

Query Match 100.0%; Score 102; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVLRKFN 21
 |||

Db 136 PRSTPSLTTKAVLVLRKFN 156

RESULT 6
 US-08-795-4738-5
 Sequence 5, 4738-5
 GENERAL INFORMATION:
 APPLICANT: Galun, Ethan
 APPLICANT: Nahot, Orli
 APPLICANT: Blum, Herbert E.
 TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 Hepatitis B Virus (HBV) Infection
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Davidson, Davidson and Kappel, LLC
 STREET: 1140 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER PROCESSABLE FORM:
 MEDIUM TYPE: 3.5 inch disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS-DOS EDITOR
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,4738
 FILING DATE: 11-FEB-1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Davidson, Clifford M.
 REGISTRATION NUMBER: 32,728
 REFERENCE/DOCKET NUMBER: 963,1007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 997-1028
 TELEFAX: (212) 997-1028
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 468 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 US-08-795-4738-5

Query Match 100.0%; Score 102; DB 4; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2e-09;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVLRKFN 21
 |||

Db 136 PRSTPSLTTKAVLVLRKFN 156

RESULT 7
 5171840-2
 Patent No. 5171840
 APPLICANT: KISHIMOTO, TADAMITSU
 TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 STIMULATORY FACTOR-2
 NUMBER OF SEQUENCES: 11

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:20 ; Search time 48.45 Seconds

Title: US-09-202-104A-11
Perfect score: 145

Scoring table:

	BLOSUM62	
Gap0	10	0
Gapext	0	5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length:	0
Maximum DB seq length:	30000000000

Post-Procure Jn: Minimum Match 09

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	100.0	458	116A_HUMAN	P08887 homo sapiens
2	121	100.0	460	116A_MOUSE	O18795 mus scrota
3	45.3	99.9	460	116A_MOUSE	P18275 mus scrota
4	47.9	99.9	462	116A_RAT	P12277 rattus norv
5	50	99.9	462	116A_RAT	P12277 rattus norv
6	49	99.9	188	P58C_RABIT	P24296 oryctolagus
7	49	99.9	188	P58C_RABIT	P24296 oryctolagus
8	49	99.9	191	B3AT_MOUSE	P32481 oryctolagus
9	47	99.9	191	B3AT_MOUSE	P32481 oryctolagus
10	46.5	99.9	344	YH8A_ECOLI	P13318 escherichia
11	46.5	99.9	344	YH8A_ECOLI	P13318 escherichia
12	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
13	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
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16	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
17	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
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26	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
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32	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia
33	46.5	99.9	344	YH8A_ECOLI	P37007 escherichia

FT DISULFID 47 92 BY SIMILARITY.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 132 132 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 374 374 A -> R (IN REF. 2).
 FT CONFLICT 374 374
 SQ SEQUENCE 460 AA: P8505908525C4 CRC64:
 Query Match 49.3% Score 72: DB 1: Length 460:
 Best Local Similarity 58.3% Pred. NO. 0.003:
 Matches 14: Conservative 2: Mismatches 8: Indels 0: Gaps 0:
 DB 129 EWHRSSTPPTTAAVLAIVKRFNS 24
 1 EWHRSSTPPTTAAVLAIVKRFNS 24
 129 EWHRSSTPPTTAAVLAIVKRFNT 152
 RESULT 4
 ID IL6A_RAT STANDARD: PRT: 462 AA.
 P22273:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-2005 (Rel. 30, Last sequence update)
 DT 01-FEB-2005 (Rel. 30, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC1_Taxid=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=EPISCHER 344; TISSUE=Liver;
 RX MEDLINE=91060602; PubMed=2174054;
 RA Baumann M., Baumann H., Fey G.H.;
 RT Molecular cloning, characterization and functional expression of the
 rat liver interleukin 6 receptor.
 RT J Biol. Chem. 265:19853-19862(1990).
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
 RA Gibson T.;
 RP Unpublished observations (FEB-1995).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 ACTIVATION REQUIRES AN ASSOCIATION WITH IL5R. ACTIVATION MAY
 LEAD TO THE REGULATION OF THE IMMUNE RESPONSE. ACUTE-PHASE
 REACTANT.
 CC -1- SIMILARITY: HEMERIN OF 2 IL6, 2 IL6F-ALPHA AND 2 IL6F7 (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 DR EMBL: M55587; AAA1431.1;
 DR PIR: A37986; A37986.
 DR HSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR001777; FN_111.
 DR InterPro: IPR003500; HematoPo_rcpfor_L_F3.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; 19-C2.
 DR EMBL: P00042; 19-C2.
 DR PIR: P00042; 19-C2.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IG2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 RX Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 RN Signal.
 RM Signal.
 FT SIGNAL 1 19
 FT SIGNAL 20 462
 FT DOMAIN 20 364
 FT TRANSMEM 365 385
 FT DOMAIN 386 462
 FT DOMAIN 40 99
 FT DISULFID 25 190
 FT DISULFID 177 192
 FT DISULFID 177 192 BY SIMILARITY.
 FT DISULFID 162 173 BY SIMILARITY.
 FT CARBOHYD 32 32 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CONFLICT 227 261
 SQ SEQUENCE 462 AA: 50398 MM: AHD064EDCC0537D CRC64:
 Query Match 47.9% Score 70: DB 1: Length 462:
 Best Local Similarity 54.2% Pred. NO. 0.006:
 Matches 13: Conservative 3: Mismatches 8: Indels 0: Gaps 0:
 DB 129 EWHRSSTPPTTAAVLAIVKRFNS 24
 1 EWHRSSTPPTTAAVLAIVKRFNS 24
 129 EWHRSSTPPTTAAVLAIVKRFNT 152
 RESULT 5
 ID RSPC_RABBIT STANDARD: PRT: 188 AA.
 P23298:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (PULMONARY
 SURFACTANT-ASSOCIATED PROTEOLIPID SP(VA)).
 GN SPFC OR SPF2.
 OS Erytholagus cuniculus (Rabbit).
 NC Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
 NC1_Taxid=9986;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Lung;
 RX MEDLINE=92351323; PubMed=1643107;
 RA Connolly I., Rossant J.;
 RT Rabbit surfactant protein C gene: alternative mRNA splicing of surfactant-associated
 protein C (SP-C) in rabbit lung.
 RT Biochim. Biophys. Acta 1127:199-207(1992).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX Bogdanin V., Margane R.K.;
 RT Rabbit surfactant protein C gene: alternative mRNA splicing of surfactant-associated
 protein C (SP-C) in rabbit lung.
 RT Am. J. Physiol. 263:1634-1644(1992).
 RN [3]
 RP SEQUENCE OF 24-188 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=9310536; PubMed=1469410.
 RX Durham P.L., Nanthakumar E.J., Snyder J.M.;
 RT Developmental regulation of surfactant-associated proteins in rabbit

HYDRA_ECOLI
AC P13518: STANDARD: PRT: 646 AA.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYDRA_ECOLI_73.3 KDA PROTEIN IN MREB-ACBP INTERGENIC REGION (F646).
GN Escherichia coli
OS Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE-97426517: PubMed-9278503;
RA Rallev M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [12]
RP SEQUENCE OF 545-646 FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE-99008079: PubMed-1049542;
RA Doi M., Machi M., Ishino F., Tomioka S., Ito M., Sakagami Y.,
RA Suzuki A., Matsubashi M.;
RA "Determinations of the DNA sequence of the mra gene and of the gene
RT products of the mra region that function in formation of the rod
RF shape of Escherichia coli cells";
RL J. Bacteriol. 170:4632-4624(1988).
CC SIMILARITY: SEQUENCE: 10.12% (HYDRA/HYDRA/XYCC FAMILY)
CC -
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DR EMBL: U16997: AAA58055.1; -
DR EMBL: AE000404: AAC76284.1; -
DR EMBL: M22055: AAA83890.1; -
DR PIR: B31843: G0CE5.
DR Ecogen: EG1018: ynda.
DR InterPro: IPR00150: DUF9.
DR Pfam: PF00563: DUF2.1.
DR Pfam: PF00990: DUF9.1.
DR SMART: SM00267: DUF2.1.
DR SMART: SM00052: DUF2.1.
DR Hypothetical protein: Complete proteome.
RW SEQUENCE 646 AA; 73339 MW; 0387E01BAC400688 CRC64;
SQ
Query Match 32.2%; Score 47; DB 1; Length 646;
Best Local Similarity 41.7%; Pred. No. 25;
Matches 10; Conservative 6; Mismatches 4; Indels 4; Gaps 1;
DB 190 EMPRISSALUT---LHFRON 209

DE HYPOHETICAL_43.8 KDA PROTEIN IN PERH-ARCP INTERGENIC REGION.
GN YACB OR B0267.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE-97426517: PubMed-9278503;
RA Blatner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE-97426517: PubMed-9278503;
RA Takemoto K., Mori H., Mureyama N., Kataoka K., Yano M., Itoh T.,
RA Mizuno T., Makino K., Nakata A., Yura T., Sempel G., Mizouchi K.,
RA Mizuno T., Makino K., Nakata A., Yura T., Sempel G., Mizouchi K.,
RA "Systematic sequencing of the Escherichia coli genome: analysis of the
RL submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RA Schramm S., Duncan M., Allen E., Araya R., Aparicio A., Chung B.,
RA Davis K., Federspiel N., Hyman R., Kallman S., Komp C., Kurdi O.,
RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RA "Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
RN [14]
RP SEQUENCE OF 245-384 FROM N.A.
RC MEDLINE-94156832: PubMed-8131168;
RA Volkart M.R., Loewen P.C., Swatlow J., Crowley D., Conley M.;
RA "The delta (arg-jac2)205(0169) deletion greatly enhances resistance
RT to hydrogen peroxide in stationary-phase Escherichia coli";
RL J. Bacteriol. 176:1197-1302(1994).
CC IDENTIFICATION.
RA Rud K.E.;
RL Unpublished observations (APR-1994).
CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 257.
CC -
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DR EMBL: E000134: AAC73370.1; -
DR EMBL: D83536: BAA77933.1; -
DR EMBL: U70243: AAB06888.1; -
DR Ecogen: EG12043: NOT_ANNOTATED_CDS.
DR InterPro: IPR001584: Yve.
DR Pfam: PF00685: Yve.1.
DR Pfam: PF00685: Yve.1.
DR Hypothetical protein: Complete proteome.
RW SEQUENCE 384 AA; 43768 MW; 96519AFACB2FED5E CRC64;
SQ
Query Match 31.8%; Score 45.5; DB 1; Length 384;
Best Local Similarity 38.9%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 9; Indels 11; Gaps 1;
DB 2 MWBPSPSLATKAVI-----LVRFQNSPA 26
DB 7 MWBPSPSLATKAVI-----LVRFQNSPA 26

[illegible]

[illegible]

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	FT	Query Match	31.8%:	Score 46.5:	DB 1:
		Best Local Similarity	46.2%:	Prel.No.75:	
		Matches 12:	Conservative 2:	Mismatches 11:	Gaps 1:
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DQ					
		766 GPASVPAY-GKATVTAQAQTGFHEH 790			
	RESULT 12				
ID	SPRR-SYNP7	STANDARD:	PRT:	257 AA.	
RN	P39663;				
DT	01-FEB-1995 (Rel. 31.)	(Created)			
AN	Cyanobacteria; Cyanobacteriales	(Taxonomic update)			
DE	01-FEB-1995 (Rel. 31.)	Last annotation update)			
DR	ALAKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTOMIAL REGULATORY PROTEIN SPRR.				
GN	SPHR.				
OS	Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).				
OX	Bacterial; Cyanobacteria; Chroococcaceae; Synechococcus.				
	NCEI_ThxID=1140:				
RN	SEQUENCE FROM N.A.				
RX	MEDLINB-91368103; PubMed-8497200;				
TX	Alba H., Nagaya M., Mizuno T.;				
RT	"Sensor and regulator proteins from the cyanobacterium Synechococcus species PCC7942 that belong to the bacterial signal-transduction protein families: implication in the adaptive response to phosphate limitation.";				
RL	J Mol Biol. 1993; 231(2):881-91.(1993).				
RP	CHARACTERIZATION.				
RZ	MEDLINB-94209219; PubMed-8157591;				
SC	Nagaya M., Alba H., Mizuno T.;				
TC	"The sprr product, a two-component system response-regulator protein,				
TT	regulates phosphate assimilation in Synechococcus sp. strain PCC 7942 by binding to the 5'-UTR upstream from the pho promoter."				
CC	-1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM SPRR/SPRS. RESPONSE REGULATOR. INVOLVED IN INDUCIBLE PRODUCTION OF ALKALINE PHOSPHATASE IN RESPONSE TO PHOSPHATE LIMITATION AS IT IS DIRECTLY INVOLVED IN THE REGULATION OF PHO _A TRANSCRIPTION IN RESPONSE TO PHOSPHATE LIMITATION. BINDS TO TWO DISTINCT SITES UPSTREAM FROM THE PHO PROMOTER.				
CC	-1- FTM: PHOSPHORYLATED BY SPRS.				
CC	-1- REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.				
CC	--				
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is acknowledged commercially or modified and this statement agreement (see http://www.isb-gib.ch/announce/or send an email to licenses@sb.slb.ch)				
CC	EMBL; D13172; BAA02453.1;				
DR	PIR; S32931; S32931.				
DR	HSSP; P03025; IODD.				
DR	InterPro; IPRO01789; Response_reg.				
DR	IPfam; PF001867; TransReg_C.				
DR	IPLink; PIPO066; TransReg_C9.1.				
DR	SMART; SM00448; REC; 1				
KW	Synthetic transduction; Phosphorylation; Transcription regulation;				
KM	DNA-binding; Activator; Phosphate transport; (BY SIMILARITY).				
MD	RES 83				
MO	SEQUENCE 257 AA.				
	3912 MW.				
	A33FE0F57044BE68 CR64;				

us-09-202-104a-11.rsp

AC 017776: 15-001-1998 (rel. 36) Created
 MC 15-001-1998 (rel. 36) Last sequence update
 DT 15-001-1998 (rel. 36) Last annotation update
 DE HYPOPHOSPHAL 41.5 KDA PROTEIN COTB7.5 IN CHROMOSOME X PRECURSOR
 GN COTB7.5.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Pelodidae; Pelidae; Genomorphida;
 OC Rhabditidae; Pelodidae; Pelidae; Genomorphida.

RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Kershaw J.;

CC -1- SIMILARITY: BELONGS TO THE DNASE II FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC
CC Ab-Duranton, D. J. Biol. Chem. 263: 1160-1164 (1988) [1987] [1988] [1989] [1990] [1991] [1992] [1993] [1994] [1995] [1996] [1997] [1998] [1999] [2000] [2001] [2002] [2003] [2004] [2005] [2006] [2007] [2008] [2009] [2010] [2011] [2012] [2013] [2014] [2015] [2016] [2017] [2018] [2019] [2020] [2021] [2022] [2023] [2024] [2025] [2026] [2027] [2028] [2029] [2030] [2031] [2032] [2033] [2034] [2035] [2036] [2037] [2038] [2039] [2040] [2041] [2042] [2043] [2044] [2045] [2046] [2047] [2048] [2049] [2050] [2051] [2052] [2053] [2054] [2055] [2056] [2057] [2058] [2059] [2060] [2061] [2062] [2063] [2064] [2065] [2066] [2067] [2068] [2069] [2070] [2071] [2072] [2073] [2074] [2075] [2076] [2077] [2078] [2079] [2080] [2081] [2082] [2083] [2084] [2085] [2086] [2087] [2088] [2089] [2090] [2091] [2092] [2093] [2094] [2095] [2096] [2097] [2098] [2099] [2100] [2101] [2102] [2103] [2104] [2105] [2106] [2107] [2108] [2109] [2110] [2111] [2112] [2113] [2114] [2115] [2116] [2117] [2118] [2119] [2120] [2121] [2122] [2123] [2124] [2125] [2126] [2127] [2128] [2129] [2130] [2131] [2132] [2133] [2134] [2135] [2136] [2137] [2138] [2139] [2140] [2141] [2142] [2143] [2144] [2145] [2146] [2147] [2148] [2149] [2150] [2151] [2152] [2153] [2154] [2155] [2156] [2157] [2158] [2159] [2160] [2161] [2162] [2163] [2164] [2165] [2166] [2167] [2168] [2169] [2170] [2171] [2172] [2173] [2174] [2175] [2176] [2177] [2178] [2179] [2180] [2181] [2182] [2183] [2184] [2185] [2186] [2187] [2188] [2189] [2190] [2191] [2192] [2193] [2194] [2195] [2196] [2197] [2198] [2199] [2200] [2201] [2202] [2203] [2204] [2205] [2206] [2207] [2208] [2209] [2210] [2211] [2212] [2213] [2214] [2215] [2216] [2217] [2218] [2219] [2220] [2221] [2222] [2223] [2224] [2225] [2226] [2227] [2228] [2229] [2230] [2231] [2232] [2233] [2234] [2235] [2236] [2237] [2238] [2239] [2240] [2241] [2242] [2243] [2244] [2245] [2246] [2247] [2248] [2249] [2250] [2251] [2252] [2253] [2254] [2255] [2256] [2257] [2258] [2259] [2260] [2261] [2262] [2263] [2264] [2265] [2266] [2267] [2268] [2269] [2270] [2271] [2272] [2273] [2274] [2275] [2276] [2277] [2278] [2279] [2280] [2281] [2282] [2283] [2284] [2285] [2286] [2287] [2288] [2289] [2290] [2291] [2292] [2293] [2294] [2295] [2296] [2297] [2298] [2299] [2300] [2301] [2302] [2303] [2304] [2305] [2306] [2307] [2308] [2309] [2310] [2311] [2312] [2313] [2314] [2315] [2316] [2317] [2318] [2319] [2320] [2321] [2322] [2323] [2324] [2325] [2326] [2327] [2328] [2329] [2330] [2331] [2332] [2333] [2334] [2335] [2336] [2337] [2338] [2339] [2340] [2341] [2342] [2343] [2344] [2345] [2346] [2347] [2348] [2349] [2350] [2351] [2352] [2353] [2354] [2355] [2356] [2357] [2358] [2359] [2360] [2361] [2362] [2363] [2364] [2365] [2366] [2367] [2368] [2369] [2370] [2371] [2372] [2373] [2374] [2375] [2376] [2377] [2378] [2379] [2380] [2381] [2382] [2383] [2384] [2385] [2386] [2387] [2388] [2389] [2390] [2391] [2392] [2393] [2394] [2395] [2396] [2397] [2398] [2399] [2400] [2401] [2402] [2403] [2404] [2405] [2406] [2407] [2408] [2409] [2410] [2411] [2412] [2413] [2414] [2415] [2416] [2417] [2418] [2419] [2420] [2421] [2422] [2423] [2424] [2425] [2426] [2427] [2428] [2429] [2430] [2431] [2432] [2433] [2434] [2435] [2436] [2437] [2438] [2439] [2440] [2441] [2442] [2443] [2444] [2445] [2446] [2447] [2448] [2449] [2450] [2451] [2452] [2453] [2454] [2455] [2456] [2457] [2458] [2459] [2460] [2461] [2462] [2463] [2464] [2465] [2466] [2467] [2468] [2469] [2470] [2471] [2472] [2473] [2474] [2475] [2476] [2477] [2478] [2479] [2480] [2481] [2482] [2483] [2484] [2485] [2486] [2487] [2488] [2489] [2490] [2491] [2492] [2493] [2494] [2495] [2496] [2497] [2498] [2499] [2500] [2501] [2502] [2503] [2504] [2505] [2506] [2507] [2508] [2509] [2510] [2511] [2512] [2513] [2514] [2515] [2516] [2517] [2518] [2519] [2520] [2521] [2522] [2523] [2524] [2525] [2526] [2527] [2528] [2529] [2530] [2531] [2532] [2533] [2534] [2535] [2536] [2537] [2538] [2539] [2540] [2541] [2542] [2543] [2544] [2545] [2546] [2547] [2548] [2549] [2550] [2551] [2552] [2553] [2554] [2555] [2556] [2557] [2558] [2559] [2560] [2561] [2562] [2563] [2564] [2565] [2566] [2567] [2568] [2569] [2570] [2571] [2572] [2573] [2574] [2575] [2576] [2577] [2578] [2579] [2580] [2581] [2582] [2583] [2584] [2585] [2586] [2587] [2588] [2589] [2590] [2591] [2592] [2593] [2594] [2595] [2596] [2597] [2598] [2599] [2600] [2601] [2602] [2603] [2604] [2605] [2606] [2607] [2608] [2609] [2610] [2611] [2612] [2613] [2614] [2615] [2616] [2617] [2618] [2619] [2620] [2621] [2622] [2623] [2624] [2625] [2626] [2627] [2628] [2629] [2630] [2631] [2632] [2633] [2634] [2635] [2636] [2637] [2638] [2639] [2640] [2641] [2642] [2643] [2644] [2645] [2646] [2647] [2648] [2649] [2650] [2651] [

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CC or send an email to license@isb-sib.ch).

DR	EMBL; Z46366; CAA66412.1; -
DR	MorMep; C07B5.5; CE00895.
KW	Hypothetical protein; signal; hydrolase.
FT	SIGNAL 1 21 POTENTIAL.
CD	33 375 HYDROLASE
ORF	C07B5 E

PT	CARBOHYD	131	131	N-TINNED (SICNAC..)	(POTENTIAL)
SQ	SEQUENCE	375 AA;	41540 MW;	E05108932919DSF	CRC64;

Best Local Similarity 33.3%; Pred. No. 19;
Matches 9; Conservative 5; Mismatches 13; Indels 0; Gaps 0

Db 110 WGSKSTSGIKLEELLSNRVYSNTHED 136
RESULT 15

ID	ITAS_HUMAN	STANDARD;	PRT;	1049 AA
AC	P08648;			
DT	01-AUG-1988	(Rel. 08, Created)		
DT	01-NOV-1988	(Rel. 09, Last sequence update)		

DE INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT)
DE (INTEGRIN ALPHA-F) (VLA-5) (CD49E).
GN ITGA5 OR ENRA.
OS Homo sapiens (Human).

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Argaves W.S., Suzuki S., Aral H., Thompson K., Pierschbacher M.D.,
RA Ruoslahti E.,
RT "Amino acid sequence of the human fibronectin receptor.",
RL J. Cell Biol. 105:1183-1190(1987).

RP SEQUENCE OF 16-1049 FROM N.A.
RX MEDLINE=88163472; PubMed=2450560;
RA Fitzgerald L.A., Poncz M., Steiner B., Rall S.C., Bennett J.S.,
Phillips D.R.;

RT fibronectin and vitronectin receptor alpha-subunits and platelet glycoprotein IIb.[†]

RT RT

RL Biochemistry 26:8158-8165(1987).

RN [3]
 RP SEQUENCE OF 821-1049 FROM N.A.
 RA MEDLINE=97008469; PubMed=2944863;
 RX Bioscience Resource Project; Fyfe R., Suzuki S., Millan J.L., Pierschbacher M.D.,
 RT "CDNA sequences from the alpha subunit of the fibronectin receptor
 RN predict a transmembrane domain and a short cytoplasmic peptide.";
 RL J. Biol. Chem. 261:12922-12924(1986).
 RE SOURCE OF 42-55; PubMed=3035641;
 RA Medline=9700441; PubMed=3035641;
 RX Thibault M., Strominger J.L., Hemler M.E.;
 RT "The very late antigen family of heterodimers is part of a
 superfamily of molecules involved in adhesion and embryogenesis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3239-3243(1987).
 CC FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN
 AND FIBRINOGEN. IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
 CC IT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
 DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
 CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
 CC -1- DATABASE: NAME=PROV. NOTE=CD guide c346 entry;
 WWW=http://www.ncbi.nlm.nih.gov/prov/cd/c346.htm"
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 modified and this statement is not removed. Usage by for commercial
 entities requires a license agreement (see http://www.isb-sib.ch/announce/
 or send an email to: license@sib-stg.ch).
 CC EMBL: X06256; CAA29601.1; -;
 DR EMBL: M13918; AAA52467.1; ALT_SEQ.
 DR PIR: A24697; A24697.
 DR PIR: A27079; E28018.
 DR PIR: E28018; E28018.
 DR HSSP: I1218; I188.
 DR DSSP: I1218; I188.
 DR MIM: 135620; P08848; -;
 DR InterPro: IP000413; Integrin_alpha.
 DR Pfam: PF01839; FG-GAP_5.
 DR Pfam: PF00357; Integrin_A_1.
 DR PRINTS: PR01185; INTEGRIN.
 DR SMART: SM00191; Int.alpha.5.
 DR SMART: SM00191; Integrin_alpha_1.
 KW Integrin cell adhesion receptor; Glycoprotein; Transmembrane;
 KW Signal; Extracellular matrix; Cytoskeleton; Calcium; Repeat.
 FT SIGNAL 1 41
 FT CHAIN 42 1049 INTEGRIN ALPHA-5 HEAVY CHAIN.
 FT CHAIN 42 894 INTEGRIN ALPHA-5 LIGHT CHAIN.
 FT CHAIN 895 1049 INTEGRIN ALPHA-5 LIGHT CHAIN.
 FT TRANSMEM 942 1021 POTENTIAL.
 FT DOMAIN 1022 1049 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 57 119 FG-GAP 1.
 FT REPEAT 131 198 FG-GAP 2.
 FT REPEAT 199 256 FG-GAP 3.
 FT REPEAT 269 322 FG-GAP 4.
 FT REPEAT 323 389 FG-GAP 5.
 FT REPEAT 390 449 FG-GAP 6.
 FT REPEAT 450 518 FG-GAP 7.
 FT CA_BIND 334 342 POTENTIAL.
 FT CA_BIND 401 409 POTENTIAL.
 FT CA_BIND 465 473 POTENTIAL.
 FT SITE 1024 1028 GEFER MOTIF.
 FT DISULFID 99 108 BY SIMILARITY.
 FT DISULFID 156 176 BY SIMILARITY.
 FT DISULFID 192 205 BY SIMILARITY.
 FT DISULFID 512 522 BY SIMILARITY.
 FT DISULFID 538 584 BY SIMILARITY.

FT DISULFID 645 651 BY SIMILARITY.
 FT DISULFID 651 651 BY SIMILARITY.
 FT DISULFID 651 651 BY SIMILARITY.
 FT DISULFID 651 651 BY SIMILARITY.
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 712 712 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 733 733 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 863 863 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 26 26 V -> L (IN REF. 2).
 FT CONFLICT 33 33 V -> L (IN REF. 2).
 SQ SEQUENCE 1049 AA; 114508 MW; C3C2CFD0B5739CBB CRC64;

Query Match 31.58; Score 46; DB 1; Length 1049;
 Desc Local Similarity 32.98; P-Value 6.3
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 DB 2 WQPSRPSITKAVLV 18
 17 WQPSRPSITKAVLV 33

Search completed: December 19, 2001, 16:26:20
 Job time: 575 sec

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DE HYPOTHETICAL PROTEIN XF2042.
 CC Xylella fastidiosa
 CC Bacteria: Proteobacteria: gamma subdivision: Xanthomonas group:
 CC Xylella.
 NC NCBITaxID=2371.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=945C. PubMed=1091047.
 RC PubMed=1091047.
 RA Simpson A.J.G. Reinach F.C. Arruda P., Abreu P.A., Acencio M.,
 RA Alvares R., Alves L.M.C., Araujo J.E., Bala G.E., Baptista C.S.,
 RA Barros M.R.P., Bonacorso E.D., Bordin S., Bove J.M., Bionas M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.P., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Falcão A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Gardner M., Goldman G., Goldman M.H.S., Gomes S.L., Guibet A.,
 RA Ho P.L., Hohensee J.D., Junqueira M.L., Kemper E.L., Kitching J.P.,
 RA Krieger J.E., Kurama E.E., Laliguet F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menezes C.F.M., Miranda E.C., Miyai C.Y., Monteiro-Vitorino C.B.,
 RA Nogueira H., Nogueira F.G., Nunes L.B., Oliveira M.A.E.S.,
 RA Nóbri A.J., Nóbri F.G., Nunes L.B., Oliveira M.A.E.S.,
 RA de Oliveira M.C., de Oliveira R.C., Palmeira D.A., Paris A.,
 RA Quaggio B.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silveira M.L.Z., Siqueira M.J., de Souza A.A.,
 RA Valade H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zeldanis J., Zetahal J.C., Vettore A.L.,
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*."
 RL EMBL: AB004021: AAF84844.1;
 RL EMBL: AB004021: AAF84844.1;
 RM Hypothetical protein; Complete proteome.
 SO SEQUENCE 242 AA; 27518 MW; AC0DECC09C9C69 CMC64;

Query Match 38.4%; Score 56; DB 2; Length 242;
 Best Local Similarity 52.4%; Pred. No. 1.2;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

3 GRRSTPSLTTRAVLVKRFON 23
 DB 44 GRLLDNTSTAVLVKRFON 64

RESULT 3
 O9FE96 PRELIMINARY; PRT; 304 AA.
 ID O9FE96
 RC O9FE96 01-JUN-2001 (TRIMBLrel. 15, Created)
 DT 01-JUN-2001 (TRIMBLrel. 16, Last sequence update)
 DE PUTATIVE RECEPTOR KINASE. 17, Last annotation update)
 OS P0463P06.5 OR OJ1212_B09.13.
 OS Oryza sativa (Rice).
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 CC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
 CC NCBITaxID=4550.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPONBARE;
 RC Sasaki T., Matsumoto T., Yamamoto K.;
 RC Oryza sativa nipponbare(GA) genomic DNA, chromosome 1, PAC
 RC Oryza sativa nipponbare(GA) genomic DNA, chromosome 1, PAC
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPONBARE;
 RC Sasaki T., Matsumoto T., Yamamoto K.;
 RC Oryza sativa nipponbare(GA) genomic DNA, chromosome 1, BAC
 RC Oryza sativa nipponbare(GA) genomic DNA, chromosome 1, BAC
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC "1. SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES."
 CC EMBL: AB004021: AAF84844.1;
 CC EMBL: AB004021: AAF84844.1;
 DR InterPro: IPR002290: Ser_Thr_kinase.
 DR InterPro: IPR002290: Ser_Thr_kinase.
 DR Pfam: PF00069: kinase. 2.
 DR SMART: SM00219: Tyr_KC. 1.
 DR SMART: SM00219: Tyr_KC. 1.
 DR PROSITE: PS0008: PROTEIN KINASE-37.1
 DR PROSITE: PS0008: PROTEIN KINASE-37.1
 KM App-binding: Kinase; Receptor; Secine/threonine-protein kinase;
 KM Transferrase
 SO SEQUENCE 304 AA; 35075 MW; 51D2AC017A9C0E CMC64;

Query Match 37.0%; Score 54; DB 10; Length 304;
 Best Local Similarity 39.1%; Pred. No. 3;
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

1 EMGRSTPSLTTRAVLVKRFON 23
 DB 265 OMNRHRSPTKTVKLVKRFON 287

RESULT 4
 O9AT05 PRELIMINARY; PRT; 638 AA.
 ID O9AT05
 RC O9AT05 01-JUN-2001 (TRIMBLrel. 17, Created)
 DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
 DE Independent evolution of orthologous at Polyploidization and
 DE LRR33.
 OS Triticum aestivum (Wheat).
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 CC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; Pooidae;
 CC Triticaceae; Triticum.
 CC NCBITaxID=4565;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=1124111;
 RC Penland A., Penland A., Gellner K., Mast A., Keller B.;
 RC "Molecular evolution of receptor-like kinase genes in hexaploid wheat."
 RC Independent evolution of orthologous at Polyploidization and
 RC Mechanisms of Local Rearrangements at Paralogous Loci."
 RL Plant Physiol. 125:1304-1313(2001).
 RL EMBL: AF325197: AAK20740.1;
 SO SEQUENCE 638 AA; 71168 MW; D54EFD39613943C5 CMC64;

Query Match 37.0%; Score 54; DB 10; Length 638;
 Best Local Similarity 39.1%; Pred. No. 6.2;
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

1 EMGRSTPSLTTRAVLVKRFON 23
 DB 599 QMNRHRSPTKTVKLVKRFON 621

RESULT 5
 O9FE96 PRELIMINARY; PRT; 663 AA.
 ID O9FE96
 RC O9FE96 01-JUN-2001 (TRIMBLrel. 15, Created)
 DT 01-JUN-2001 (TRIMBLrel. 16, Last sequence update)

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RESULT 12
ID 09F004 PRELIMINARY PRT: 635 AA.
AC 09F001:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698603.29.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
NCBI_TaxID=4530.
RM [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RC clone: p0698603; apportionate(GA3) genomic DNA, chromosome 1, PAC
FL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AP002747; BAB17345.1.
DE Interpro: IPR000719; Euk-kinase.
DR Interpro: IPR002290; Set_thr_kin_actsite.
DR Interpro: IPR001245; Tyr_kin.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00219; S_TKc; 1.
DR SMART: SM00219; S_TKc; 1.
DR SMART: SM00219; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 635 AA: 711/1 MW: 64692134f6f1b83 CRC64:
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Query Match 34.9%; Score 51; DB 10; Length 635;
Best local similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0:

OY 1 EMGPSPELTITKAVILVRFKN 23
DB 596 QANPNRPSMTKXVNMILGRQN 618

RESULT 13
ID 09FT28 PRELIMINARY PRT: 636 AA.
AC 09FT28:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698603.32.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
NCBI_TaxID=4530.
RM [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RC clone: p0698603; apportionate(GA3) genomic DNA, chromosome 1, PAC
FL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AP002747; BAB17345.1.
DE Interpro: IPR000719; Euk-kinase.
DR Interpro: IPR002290; Set_thr_kin_actsite.
DR Interpro: IPR001245; Tyr_kin.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00219; S_TKc; 1.
DR SMART: SM00219; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 643 AA: 715/1 MW: 64692134f6f1b83 CRC64:
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DR SMART: SM00220; S_TKc; 1.
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DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR SMART: SM00219; S_TKc; 1.
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SQ SEQUENCE 636 AA: 705/6 MW: 65805991d43462 CRC64:
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Query Match 34.9%; Score 51; DB 10; Length 636;
Best local similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0:

OY 1 EMGPSPELTITKAVILVRFKN 23
DB 588 QANPNRPSMTKXVNMILGRQN 610

RESULT 14
ID 09F004 PRELIMINARY PRT: 643 AA.
AC 09F004:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698603.26.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
NCBI_TaxID=4530.
RM [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RC clone: p0698603; apportionate(GA3) genomic DNA, chromosome 1, PAC
FL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AP002747; BAB17342.1.
DE Interpro: IPR000719; Euk-kinase.
DR Interpro: IPR002290; Set_thr_kin_actsite.
DR Interpro: IPR001245; Tyr_kin.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00219; S_TKc; 1.
DR SMART: SM00219; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 643 AA: 715/25 MW: BBP45CB172A6F15A CRC64:
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Query Match 34.9%; Score 51; DB 10; Length 643;
Best local similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0:

OY 1 EMGPSPELTITKAVILVRFKN 23
DB 604 QANPNRPSMTKXVNMILGRQN 626

RESULT 15
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AC 09F84:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698603.1 OR P0463906.20.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Genome version 4.5
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OK protein - protein search, using SW model

Run on: December 19, 2001, 16:21:03 ; Search time 78.52 seconds
(without alignments)
8.025 Million coll updates/sec

Title: US-09-202-104a-11

Perfect score: 1 EMBRSTPSLTITKAVLVKRFQNSPAD 28

Sequence: 1 EMBRSTPSLTITKAVLVKRFQNSPAD 28

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 21252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 21252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2.6/prodata/2/1aa/5A.COMB.pep:*
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- 3: /cgn2.6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2.6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2.6/prodata/2/1aa/6C.COMB.pep:*
- 6: /cgn2.6/prodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB	ID	Description
1	146	100.0	210	4	US-09-043-785-1	Sequence 1, Appl1
2	146	100.0	323	6	5171840-6	Patent No. 5171840
3	146	100.0	323	6	5480796-6	Patent No. 5480796
4	146	100.0	344	6	5171840-7	Patent No. 5171840
5	146	100.0	344	6	5480796-5	Patent No. 5480796
6	146	100.0	468	6	5171840-2	Patent No. 5171840
7	146	100.0	468	6	5480796-2	Patent No. 5480796
8	146	100.0	468	6	5171840-5	Patent No. 5171840
9	119	81.5	386	6	5171840-5	Patent No. 5171840
10	119	81.5	386	6	5480796-5	Patent No. 5480796
11	114	78.1	201	6	5171840-11	Sequence 7, Appl1
12	114	78.1	201	6	5480796-11	Sequence 7, Appl1
13	114	78.1	201	6	5171840-11	Sequence 7, Appl1
14	114	78.1	201	6	5480796-11	Sequence 7, Appl1
15	114	78.1	201	6	5171840-11	Sequence 7, Appl1
16	114	78.1	201	6	5480796-11	Sequence 7, Appl1
17	114	78.1	201	6	5171840-11	Sequence 7, Appl1
18	114	78.1	201	6	5480796-11	Sequence 7, Appl1
19	114	78.1	201	6	5171840-11	Sequence 7, Appl1
20	114	78.1	201	6	5480796-11	Sequence 7, Appl1
21	114	78.1	201	6	5171840-11	Sequence 7, Appl1
22	114	78.1	201	6	5480796-11	Sequence 7, Appl1
23	114	78.1	201	6	5171840-11	Sequence 7, Appl1
24	114	78.1	201	6	5480796-11	Sequence 7, Appl1
25	114	78.1	201	6	5171840-11	Sequence 7, Appl1
26	114	78.1	201	6	5480796-11	Sequence 7, Appl1
27	114	78.1	201	6	5171840-11	Sequence 7, Appl1

28	42	28.8	682	4	US-09-099-639-107	Sequence 107, App
29	42	28.8	682	5	PCT-US93-12588-107	Sequence 107, App
30	42	28.8	682	5	PCT-US93-08071-107	Sequence 107, App
31	42	28.8	682	5	PCT-US93-08071-107	Sequence 107, App
32	42	28.8	682	5	PCT-US93-08071-107	Sequence 107, App
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34	42	28.8	682	5	PCT-US93-08071-107	Sequence 107, App
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ALIGNMENTS

RESULT 1
US-09-043-785-1

Sequence 1, Application US/09043785

Patent No. 6172042

APPLICANT: CHISHIMOTO, Tadashi

APPLICANT: HAKIMI, Hubert

APPLICANT: REVEL, Michel

TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY

CURRENT APPLICATION NUMBER: US/09/043,785

CURRENT FILING DATE: 1995-09-02

EARLIER APPLICATION NUMBER: US/09-026/00119

EARLIER FILING DATE: 1995-09-26

EARLIER APPLICATION NUMBER: 115,453

EARLIER FILING DATE: 1995-09-26

EARLIER APPLICATION NUMBER: 118,097

EARLIER FILING DATE: 1996-05-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ LENGTH: 210

TYPE: PRT

ORGANISM: Human

US-09-043-785-1

Query Match: 100.0%, Score 146, DB 4, Length 210.

Matches: 28; Conservative 100.0%, Mismatches 0, Indels 0, Gaps 0;

DB 21 EMBRSTPSLTITKAVLVKRFQNSPAD 48

RESULT 2

Patent No. 5171840

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 11

APPLICATION NUMBER: DATA

FILING DATE: 19-JAN-1989

SEQ ID NO:6

LENGTH: 323

5171840-6

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; APPLICANT: KISHIMOTO, YADAMITSU
;
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
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; NUMBER OF SEQUENCES: 11
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298, 694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2
; LENGTH: 468
5171840-2

Query Match
Best Local Similarity 100.0%; Score 146; DB 6; Length 468;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGGPSTPSLTTRAVLVRRFONSPAD 28
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DB 133 EGGPSTPSLTTRAVLVRRFONSPAD 160

RESULT 8
5480796-2
Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907, 650
; FILING DATE: 02-JUL-1992
; PRIORITY DATE: 19-JAN-1989
; APPLICATION NUMBER: 298, 694
; SEQ ID NO:2
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11
; LENGTH: 468
5480796-2

Query Match
Best Local Similarity 100.0%; Score 146; DB 6; Length 468;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGGPSTPSLTTRAVLVRRFONSPAD 28
    |||||||
DB 133 EGGPSTPSLTTRAVLVRRFONSPAD 160

RESULT 9
5171840-5
Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298, 694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5
; LENGTH: 386
5171840-5

Query Match
Best Local Similarity 81.5%; Score 119; DB 6; Length 386;
Matches 26; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 GPRSTP--SLTTRAVLVRRFONSPAD 28
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DB 51 GPRSTPMSLTTRAVLVRRFONSPAD 78

RESULT 10
5480796-5
Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
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; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907, 650
; FILING DATE: 02-JUL-1992
; PRIORITY DATE: 19-JAN-1989
; APPLICATION NUMBER: 298, 694
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; FILING DATE: 19-JAN-1989
; SEQ ID NO:11
; LENGTH: 386
5480796-5

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Best Local Similarity 81.5%; Score 119; DB 6; Length 386;
Matches 26; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 GPRSTP--SLTTRAVLVRRFONSPAD 28
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DB 51 GPRSTPMSLTTRAVLVRRFONSPAD 78

RESULT 11
5171840-11
Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298, 694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11
; LENGTH: 201
5171840-11

Query Match
Best Local Similarity 78.1%; Score 114; DB 6; Length 201;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 11 EGGPSTPSLTTRAVLVRRFO 32

RESULT 12
US-08-160-524A-7
; Sequence 7, Application US/08160524A
; Patent No. 5851761
; GENERAL INFORMATION:
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; TITLE OF INVENTION: PROBES, KITS AND METHODS FOR THE
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; COMPUTER READABLE FORM:
; METHOD: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160, 524A
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